

Sample Bank

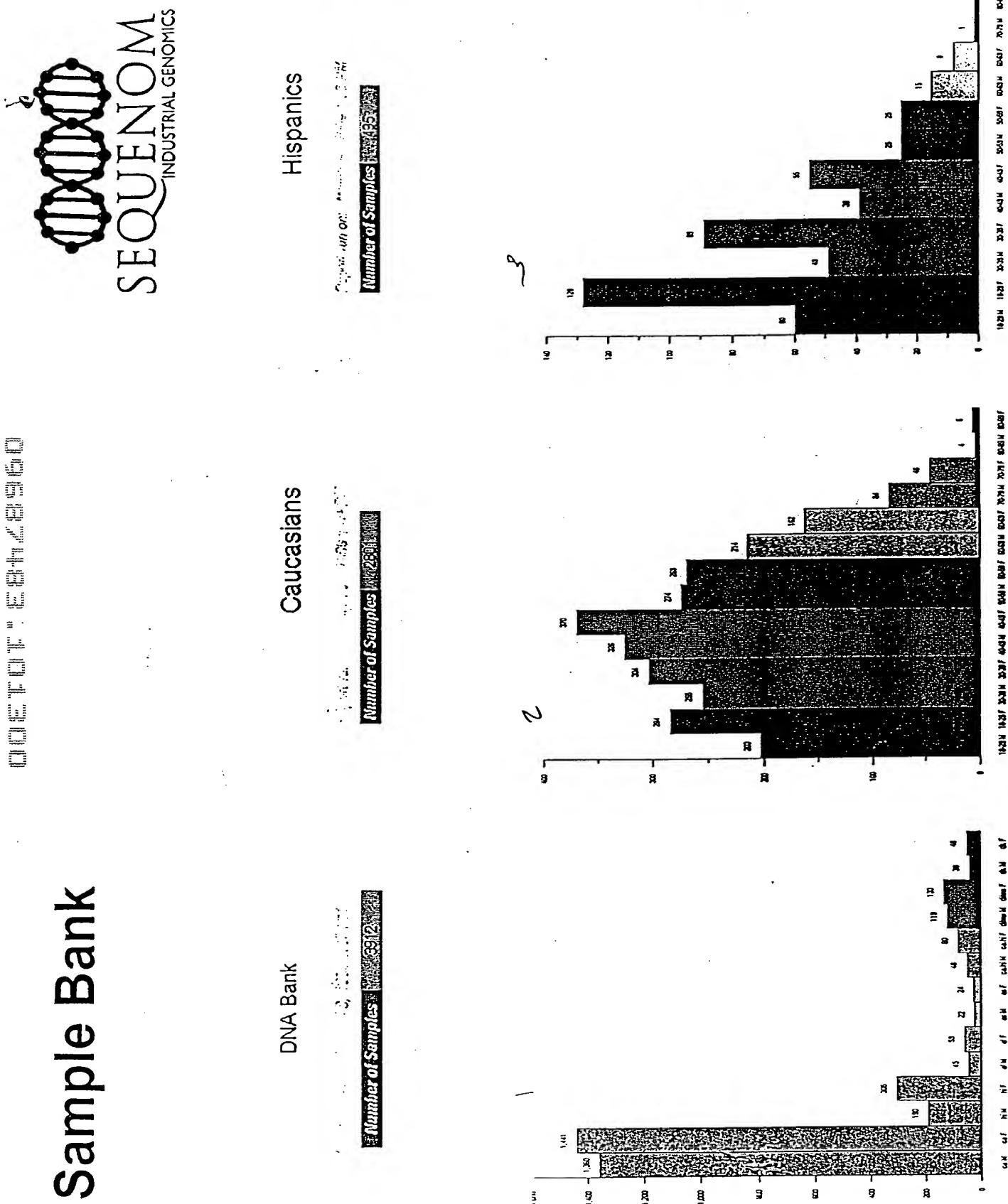


FIGURE 1

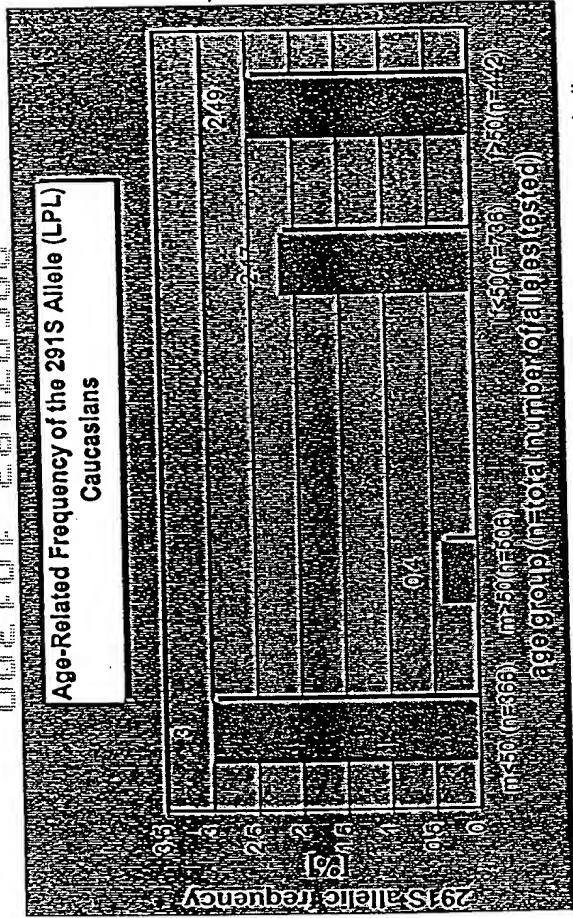


FIGURE 2A

age- and sex-distribution of the 291S allele of the lipoprotein lipase gene. A total of 436 males and 589 females were investigated.

Age-related distribution of the 291S allele of the lipoprotein lipase gene within the

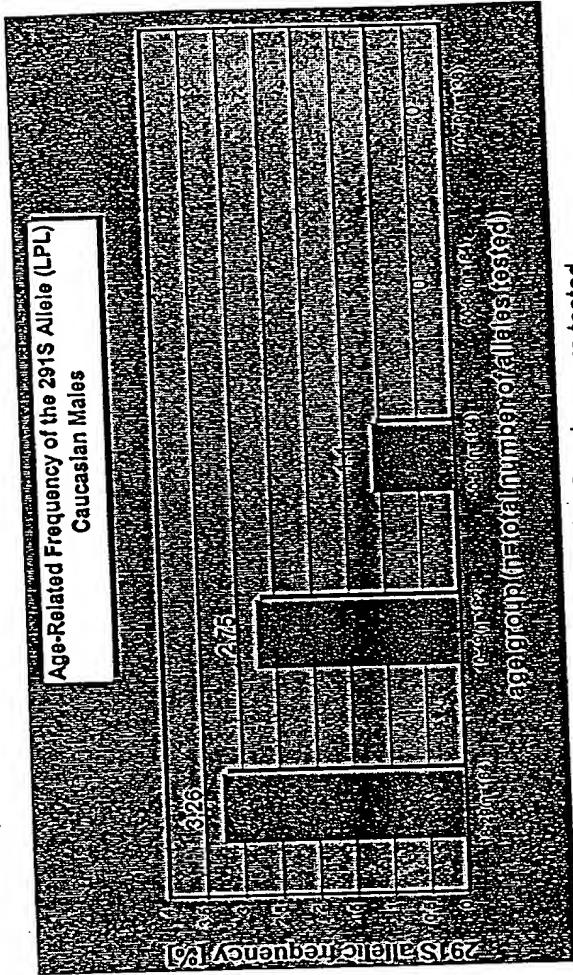
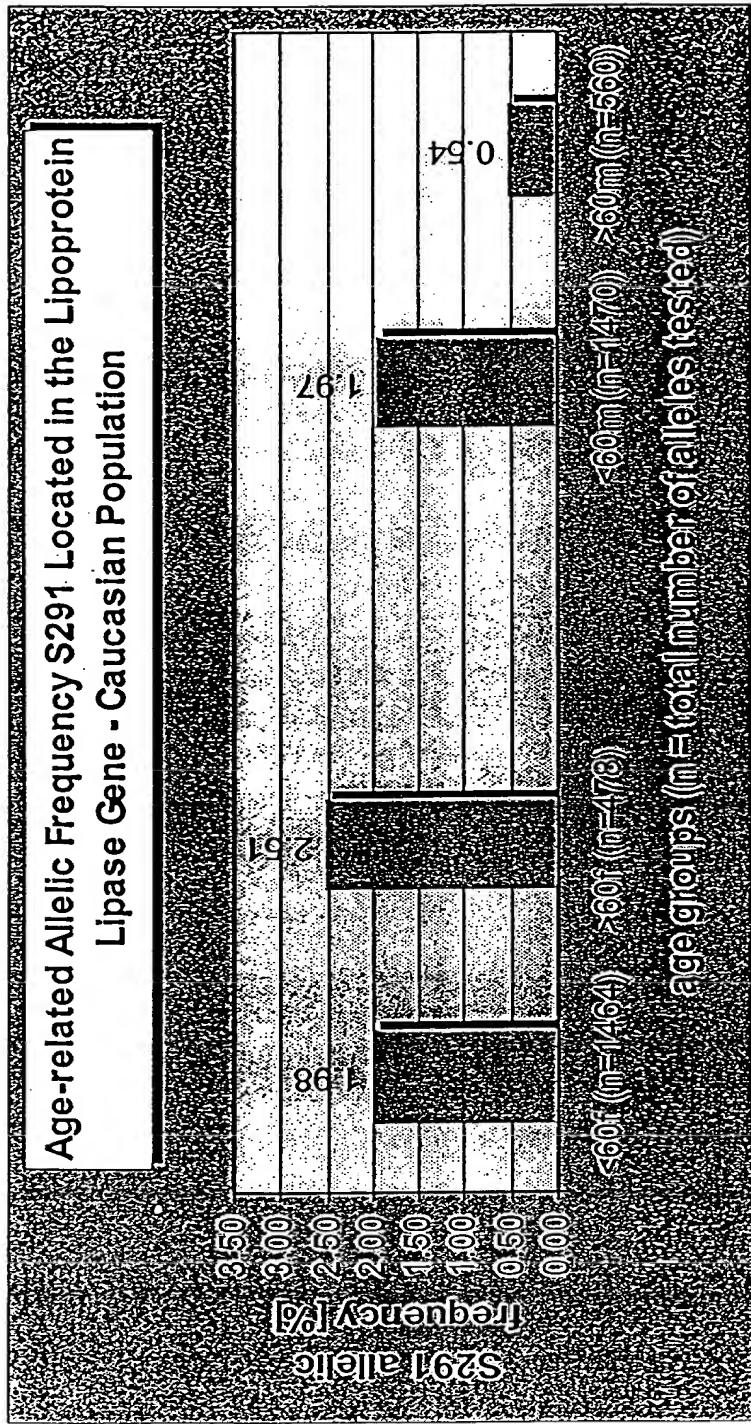


FIGURE 2B

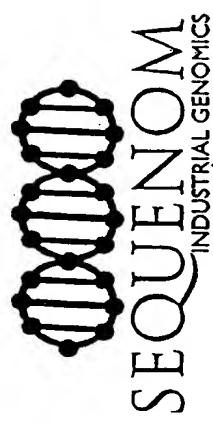
male Caucasian population. A total of 436 males were tested.



Significance: Allele frequency of Ser291 drops from 1.97% to 0.54% in males; $p=0.009$

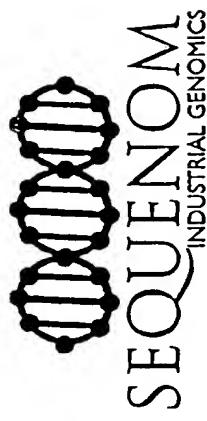
FIGURE 2C

Intelligent Genomics



Questionnaire for Population-Based Sample Banking

FIGURE 3



Intelligent Genomics

Sample Banks

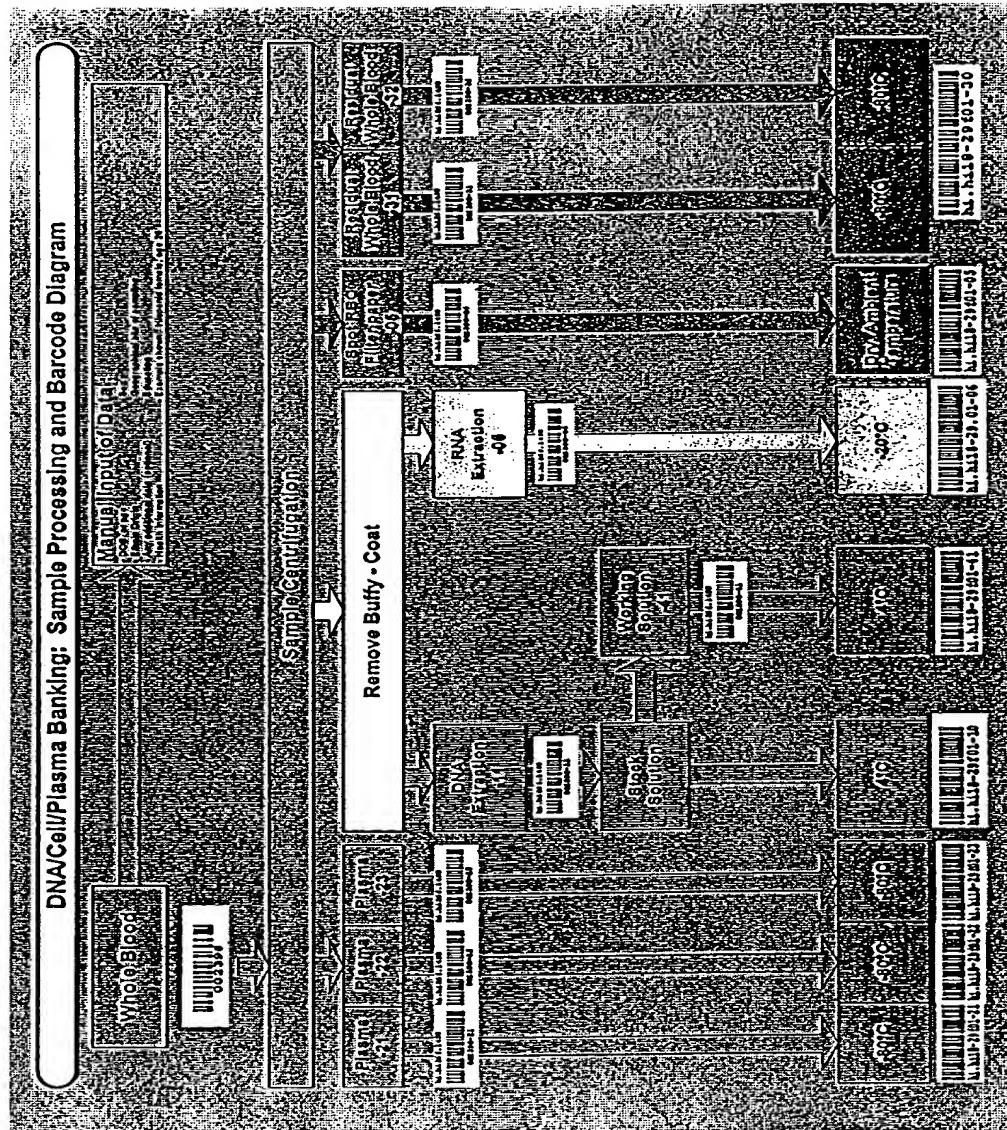


FIGURE 4

Intelligent Genomics

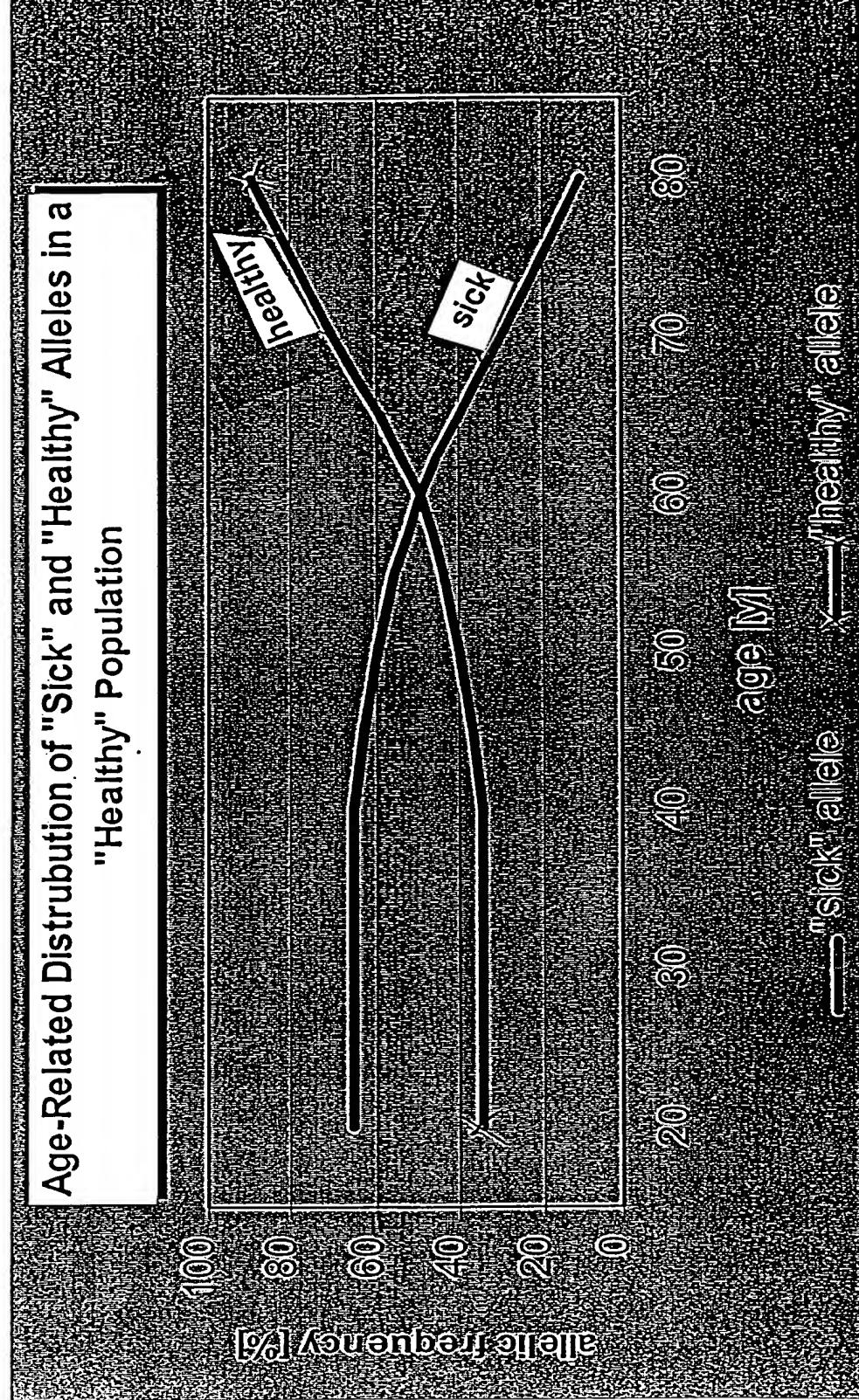
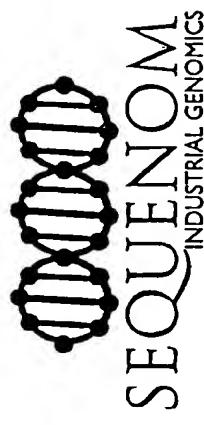
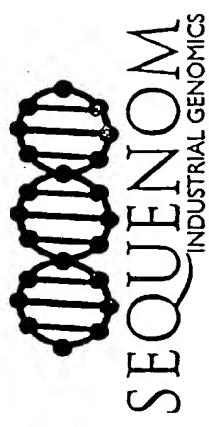


FIGURE 5

Intelligent Genomics



Age-Dependent Distribution of ApoE Genotypes / Alleles

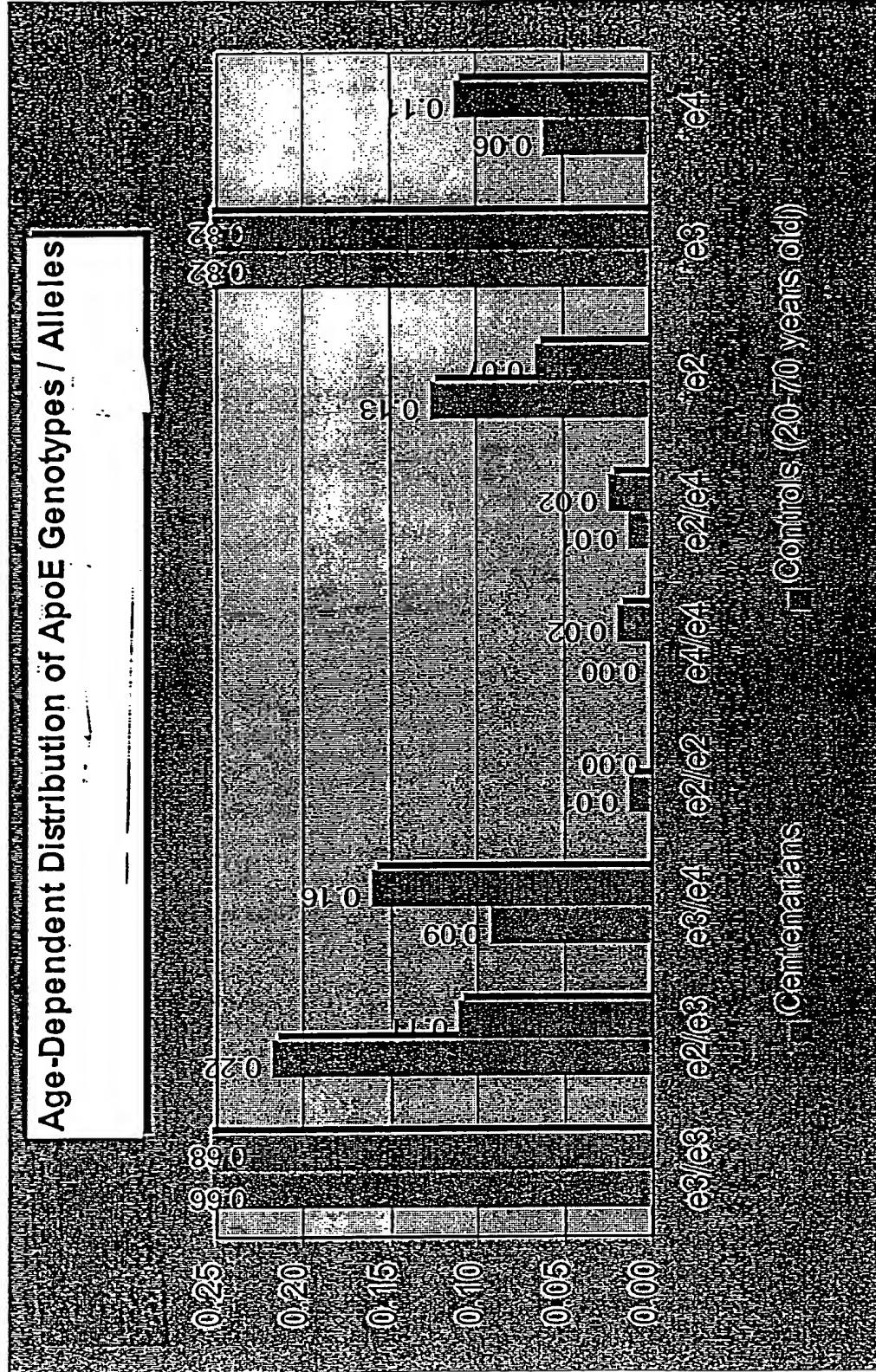
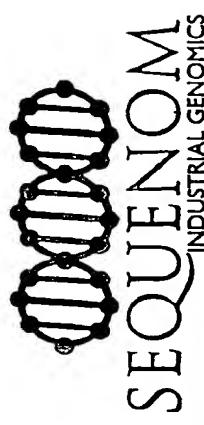
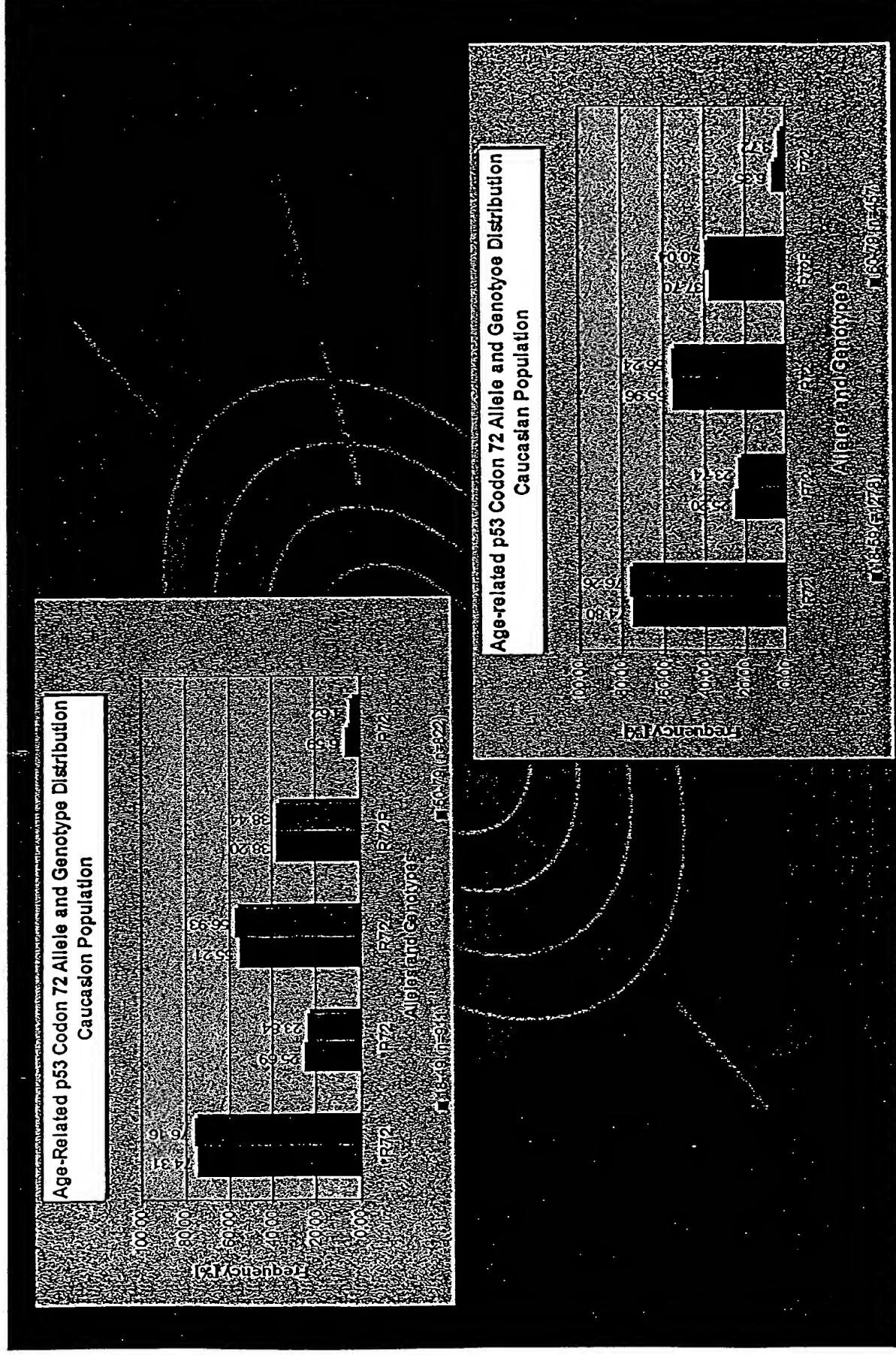


FIGURE 6

FIGURE 7A



1 Genotypes



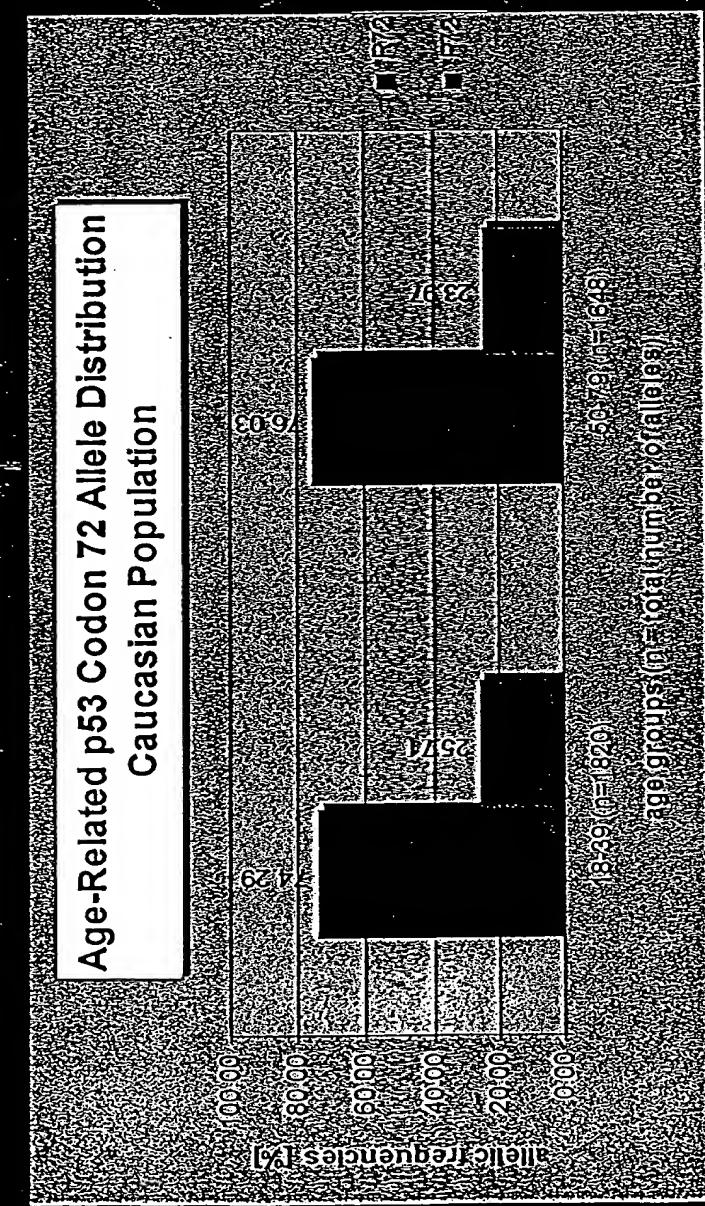


FIGURE 7B

Allele Distribution among Different Ethnic Groups
Själlander et al. *Hum Hered* 46: 41-48, 1996

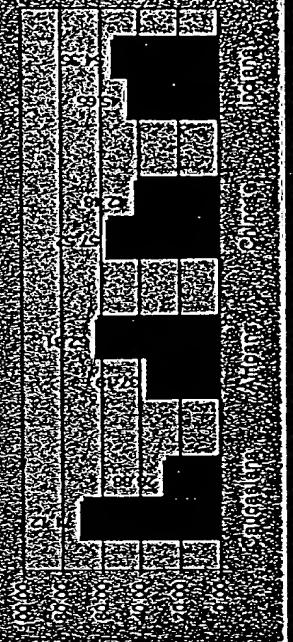
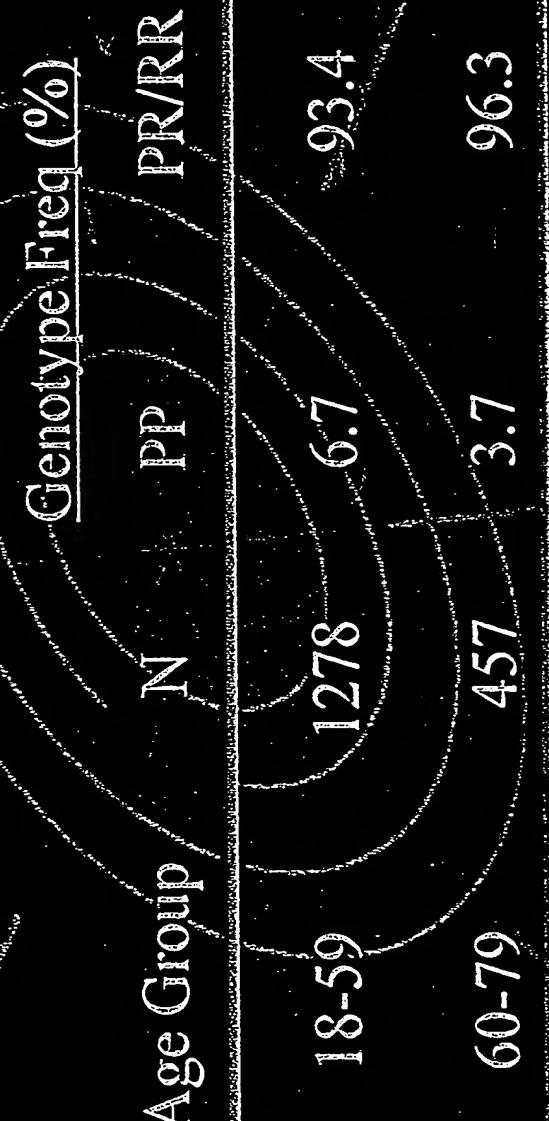


FIGURE 7C

i genetics

P53 PP vs. PR/RR Genotype Distribution

By Age cut point = 59



00000000000000000000000000000000

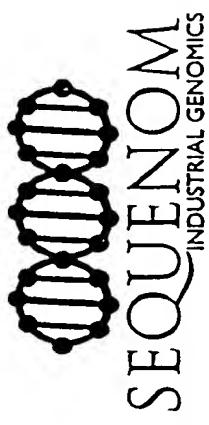
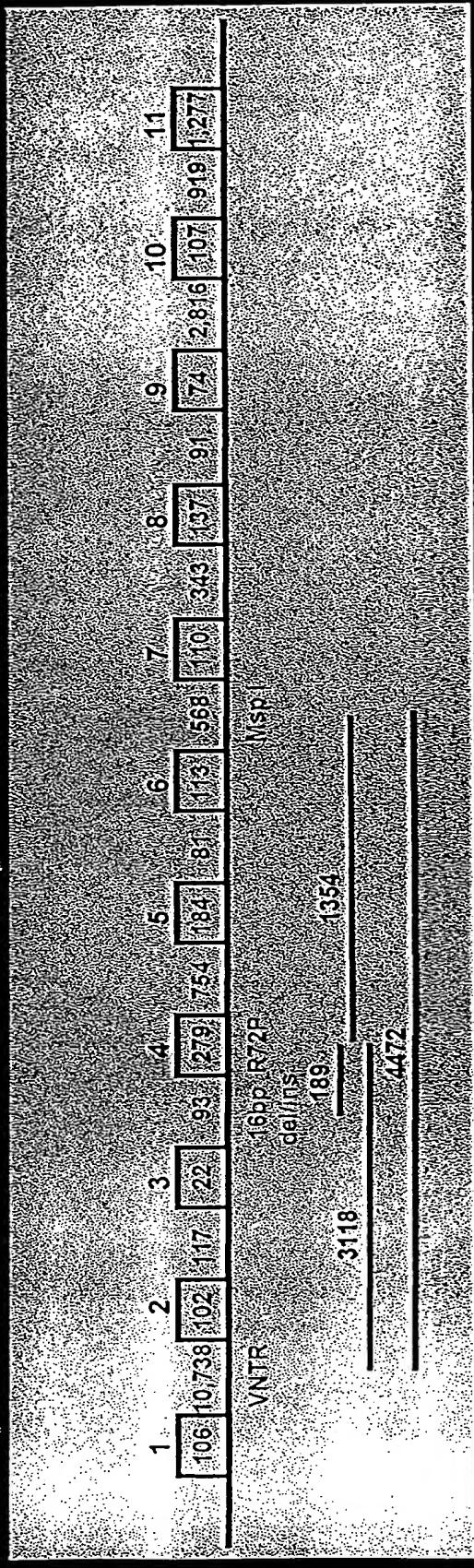
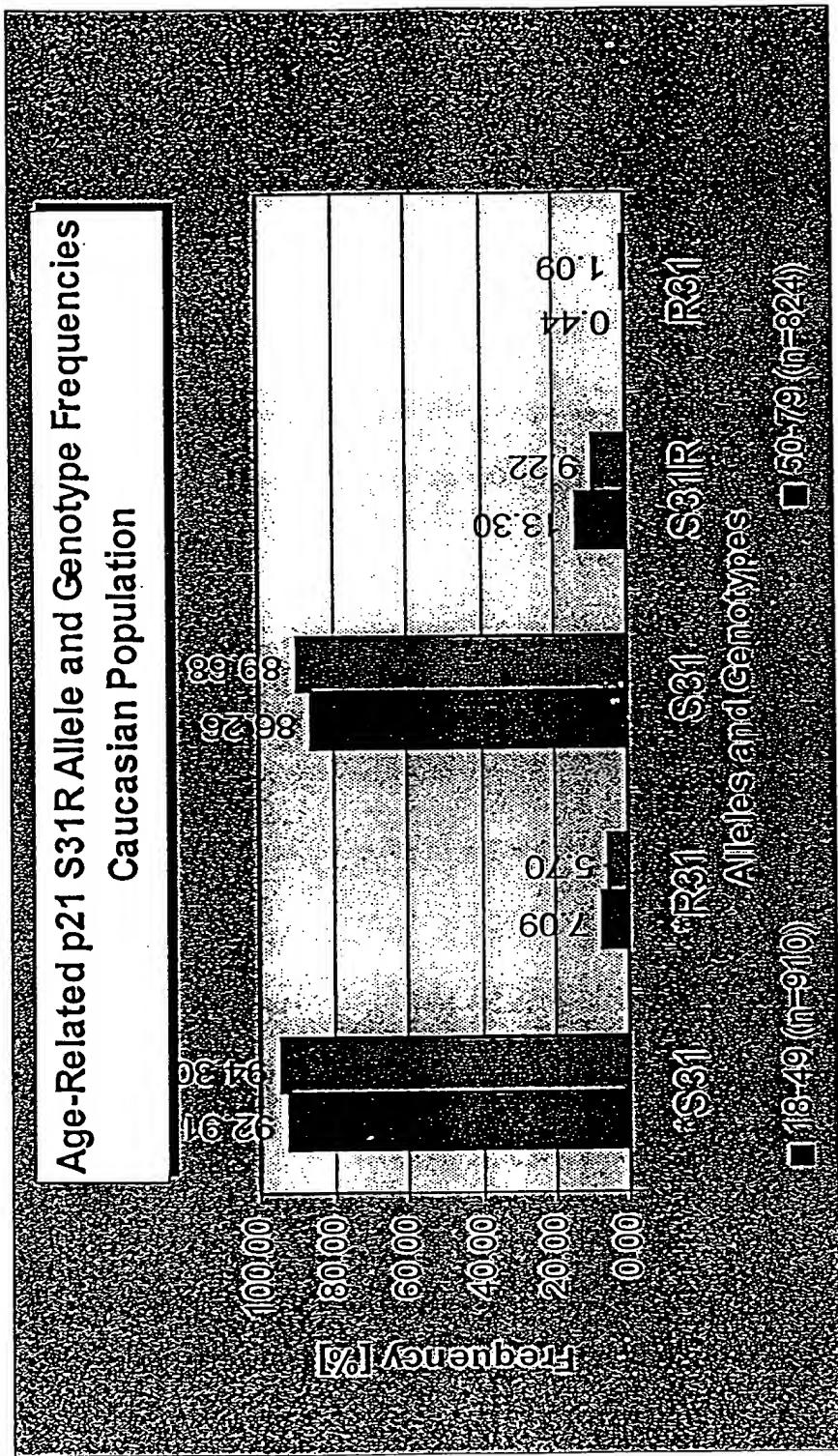


FIGURE 7D

Genomic Organization of the p53 Gene





Significance: Genotype frequency of SR heterozygous drops from 13.3% to 9.2%; $p=0.009$

FIGURE 8

DRAFTS OF THE CONSTITUTION OF THE UNITED STATES

DNA MassArray™

FVII R353Q

SEQUENOM
INDUSTRIAL GENOMICS

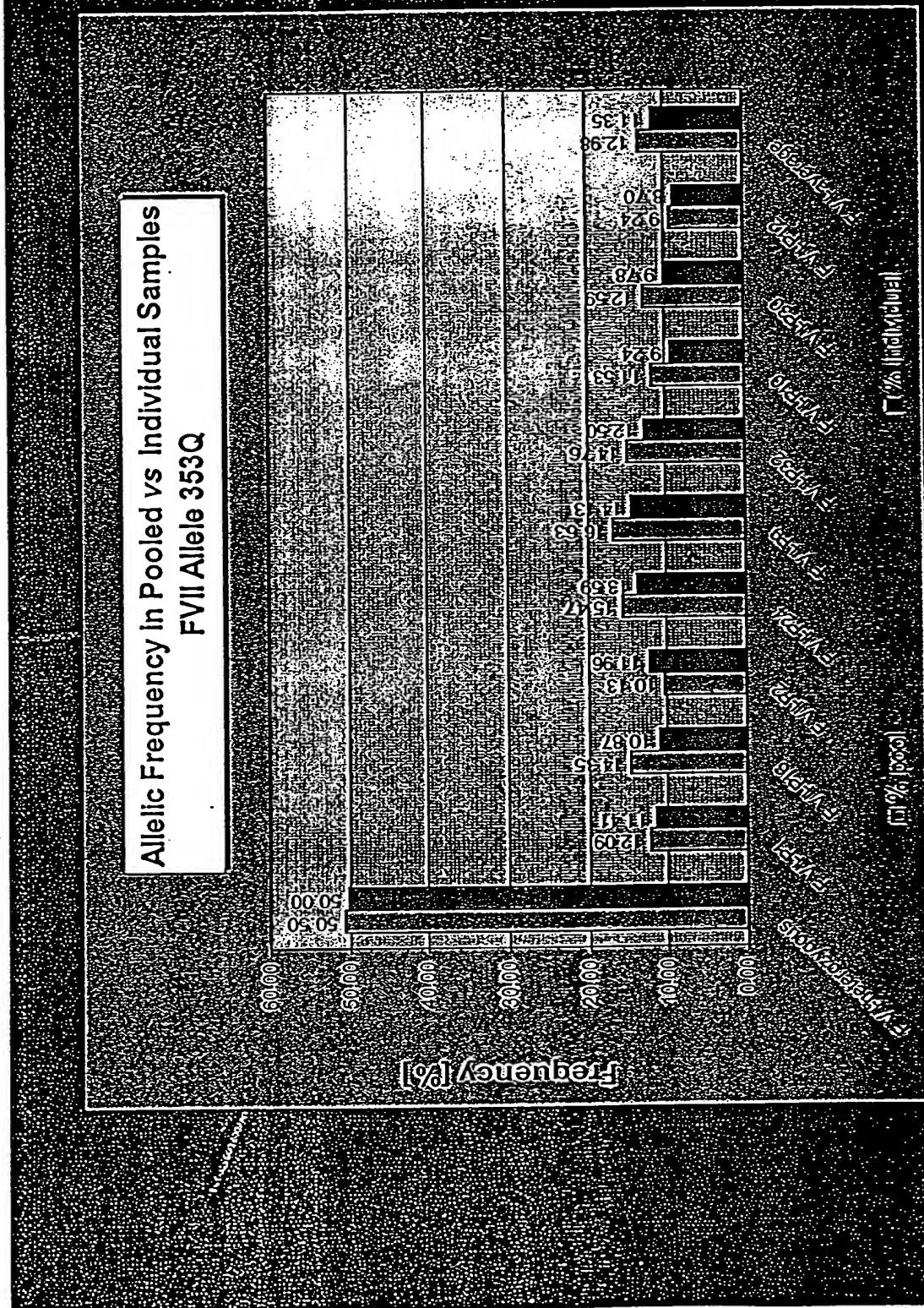


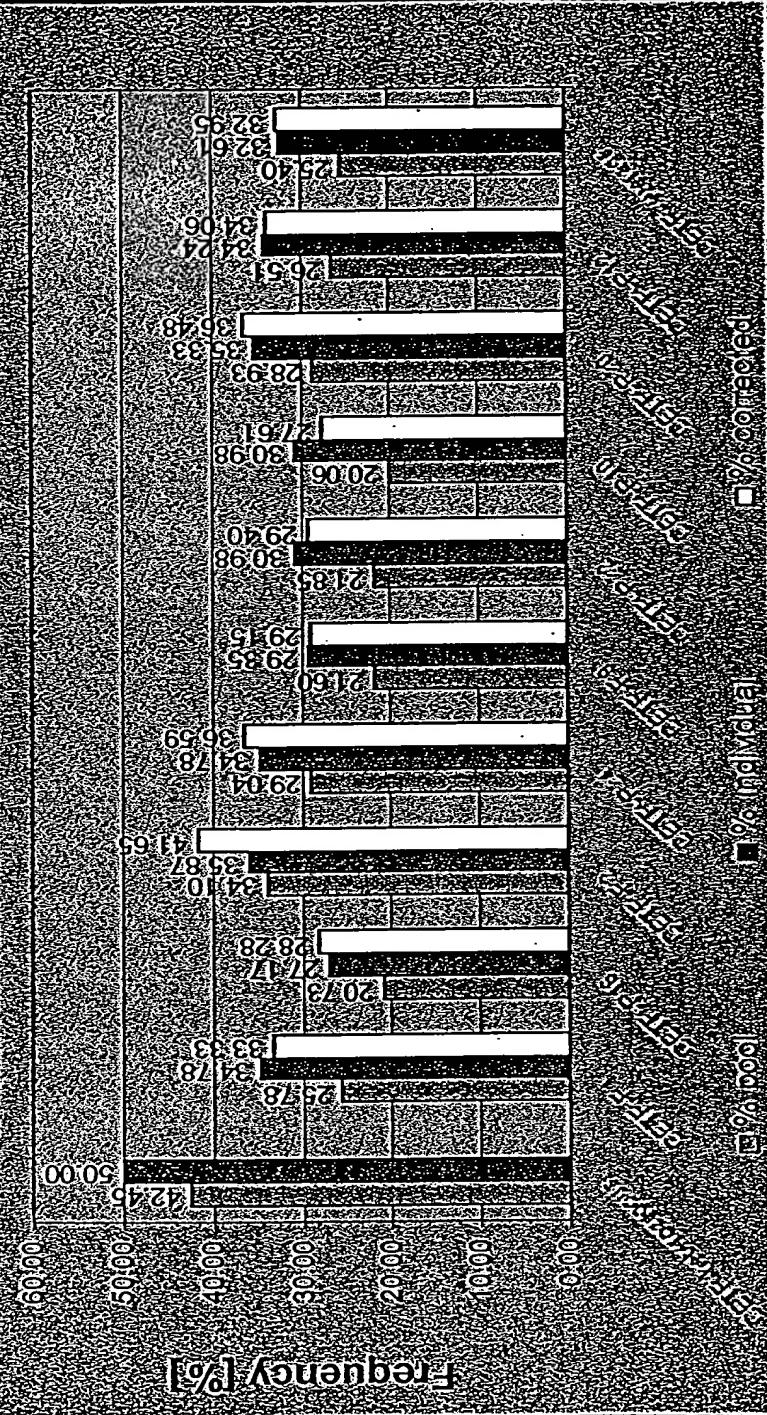
FIGURE 9

DNA MassArray™ CETP I405V

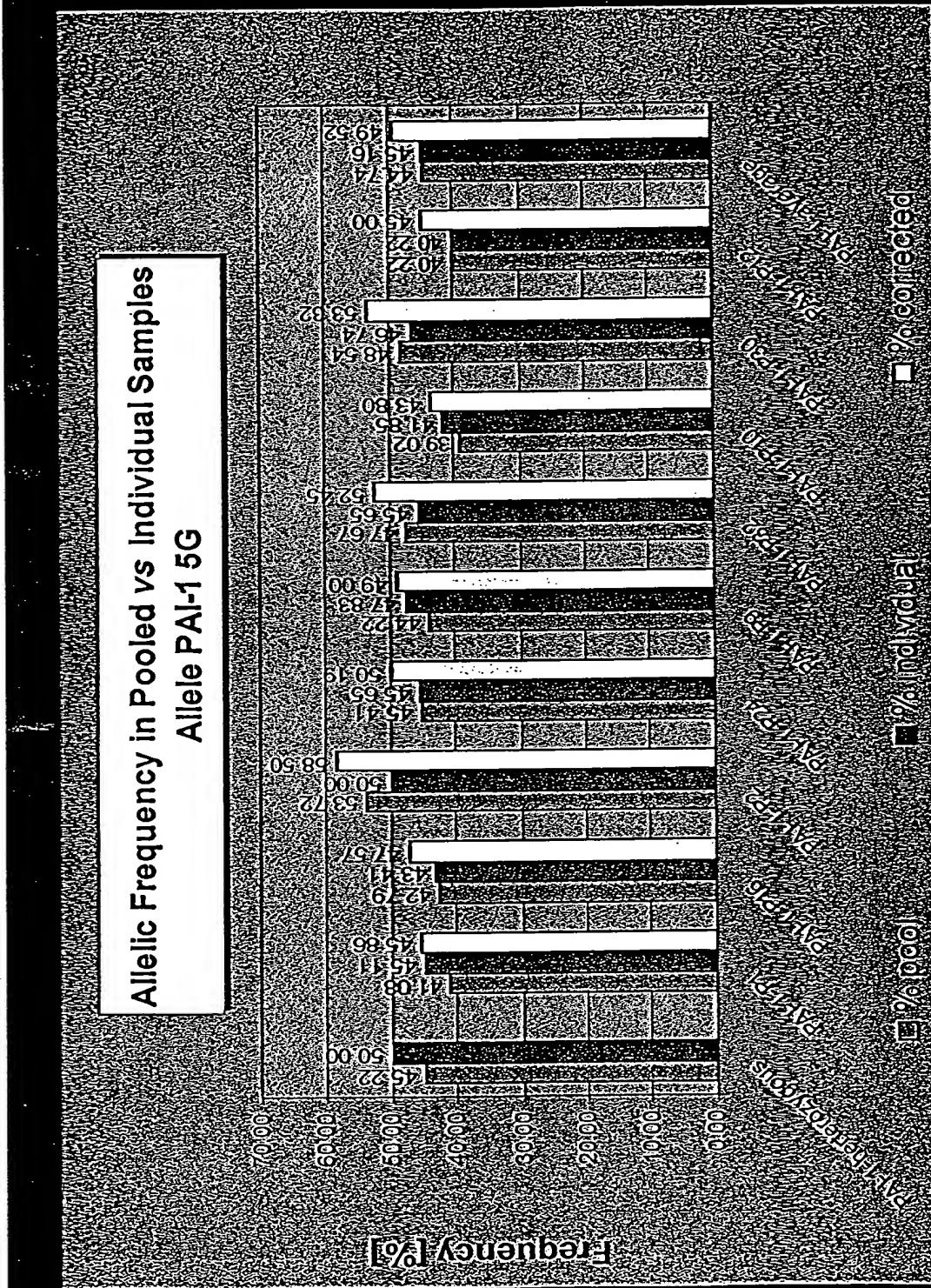
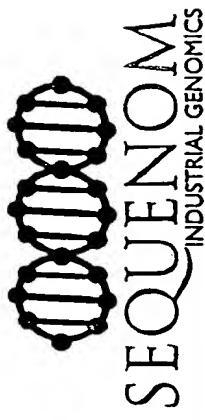
SEQUENOM
INDUSTRIAL GENOMICS

0022701-23428950

Allelic Frequency in Pooled vs Individual Samples CETP Allele 405V



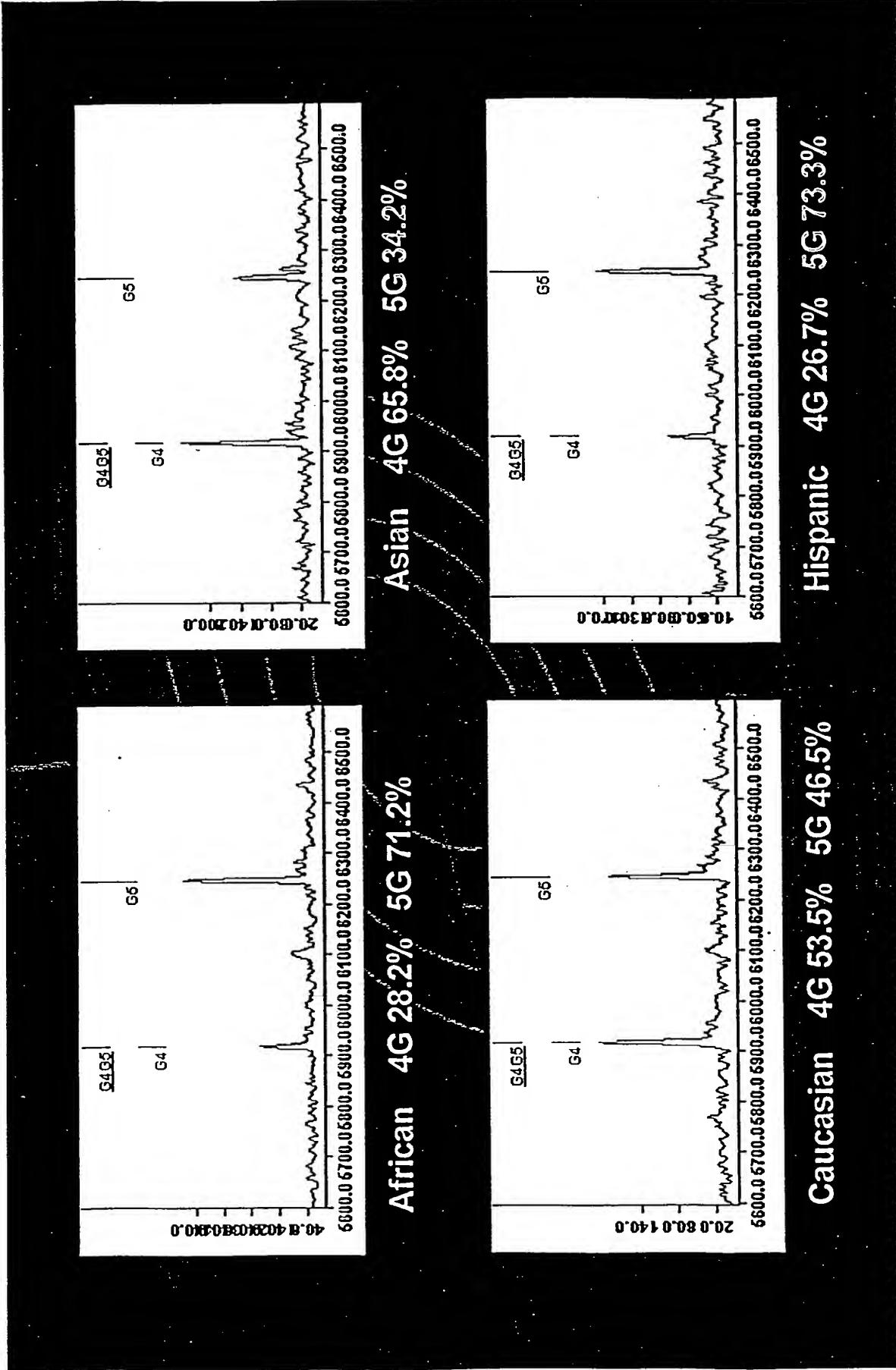
DNA MassArray™ PAI-1 4G/5G



DNA MassArray™

Ethnic Diversity (PAI-1)

SEQUENOM
INDUSTRIAL GENOMICS



DNA MassArray™

Ethnic Diversity (CETP 405)

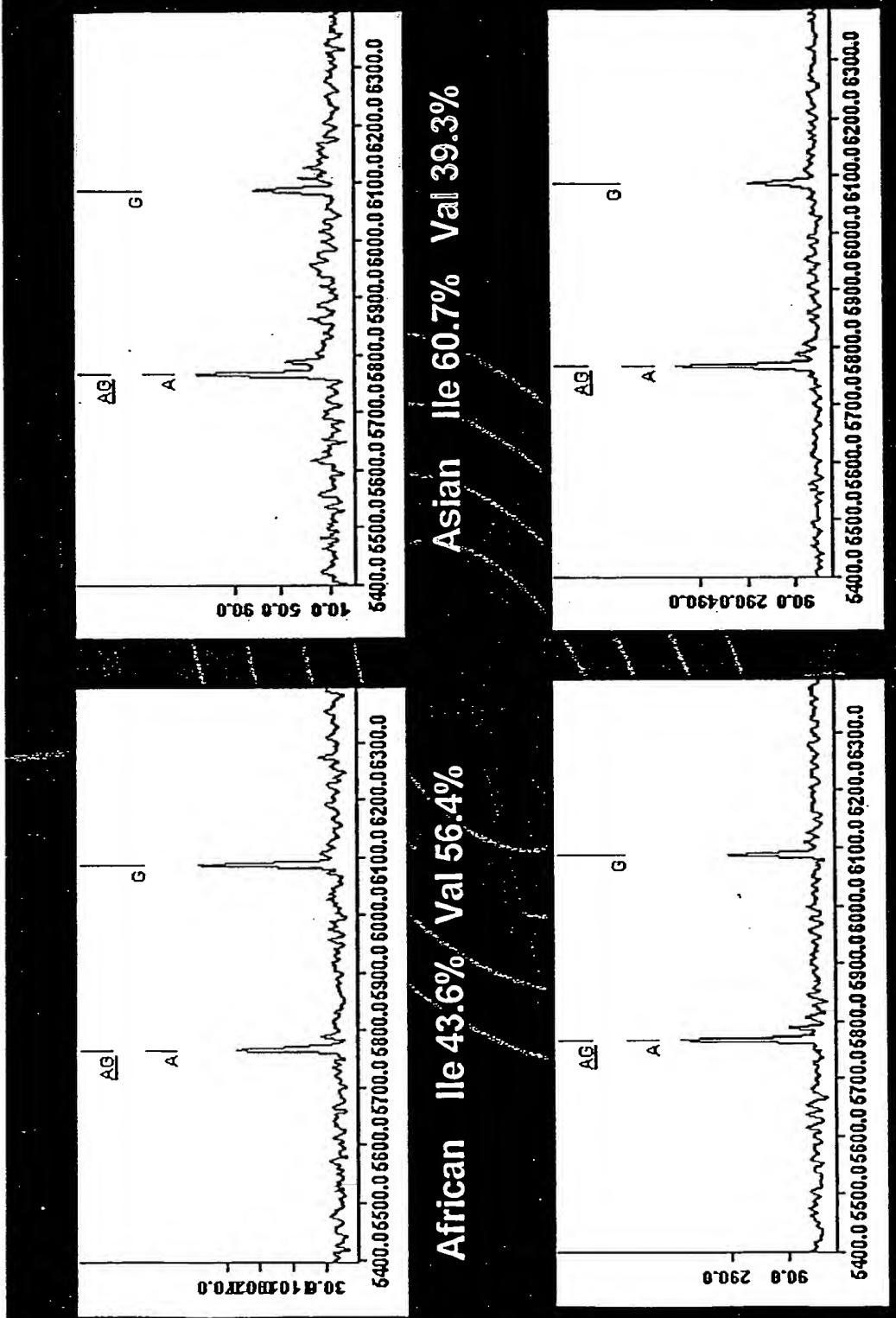
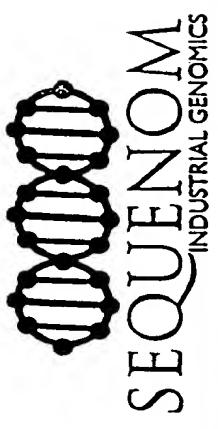


FIGURE 13

DNA MassArray™

Ethnic Diversity (Factor VII 353)

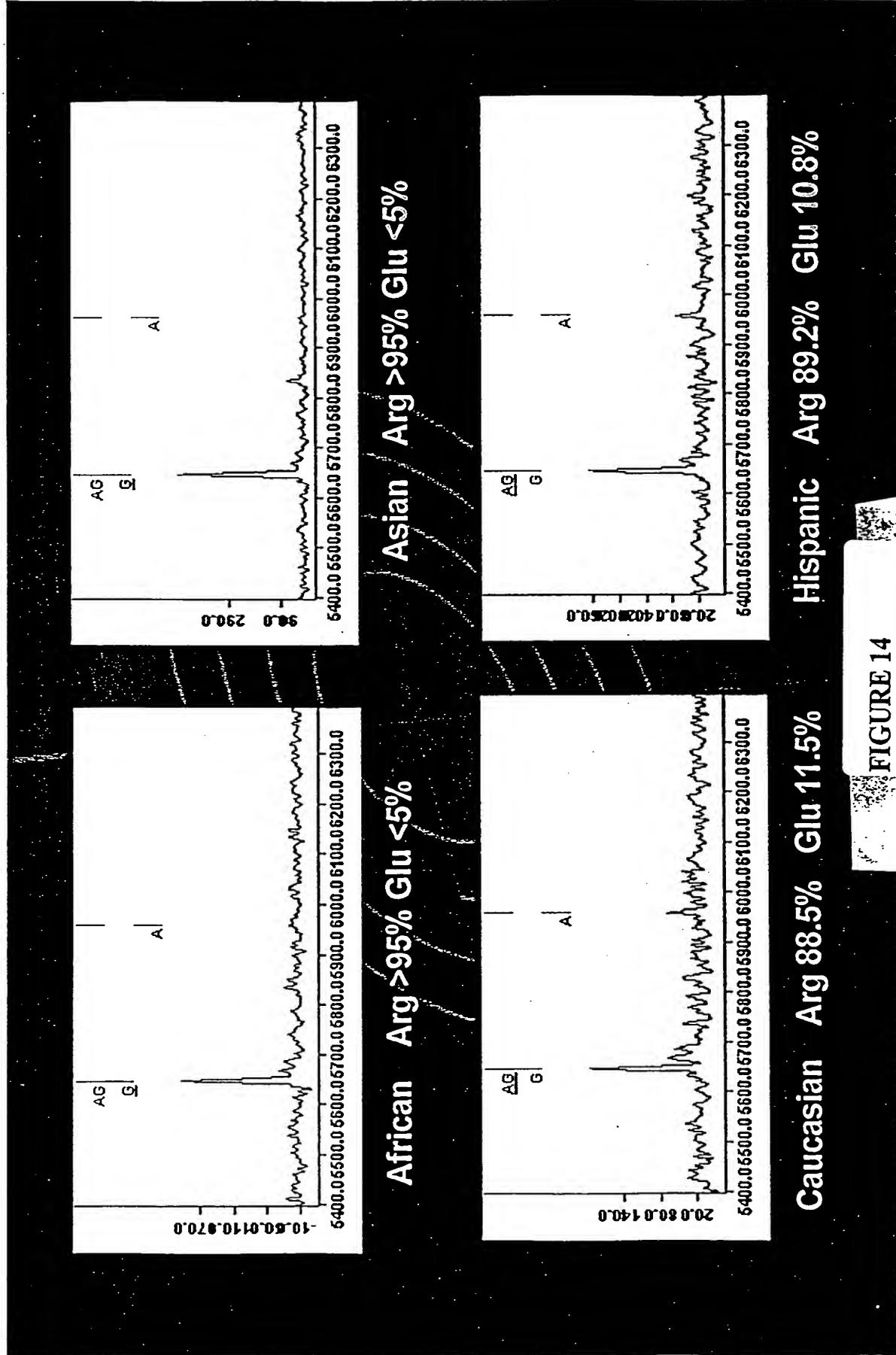
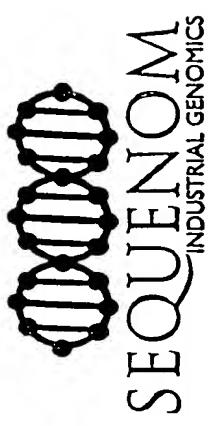


FIGURE 14

DNA MassArray™

Ethnic Diversity



Ethnic diversity using pooled DNA samples

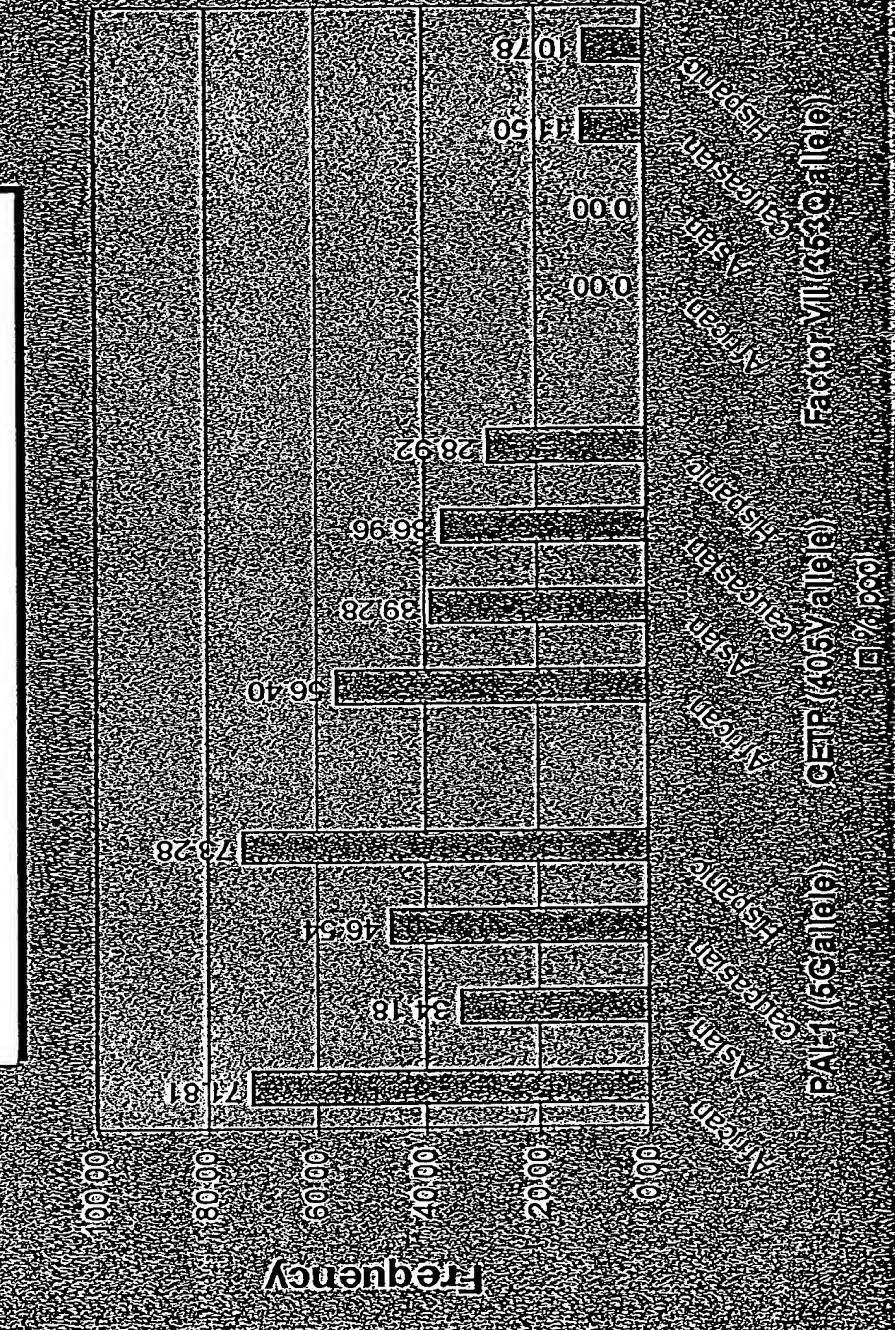
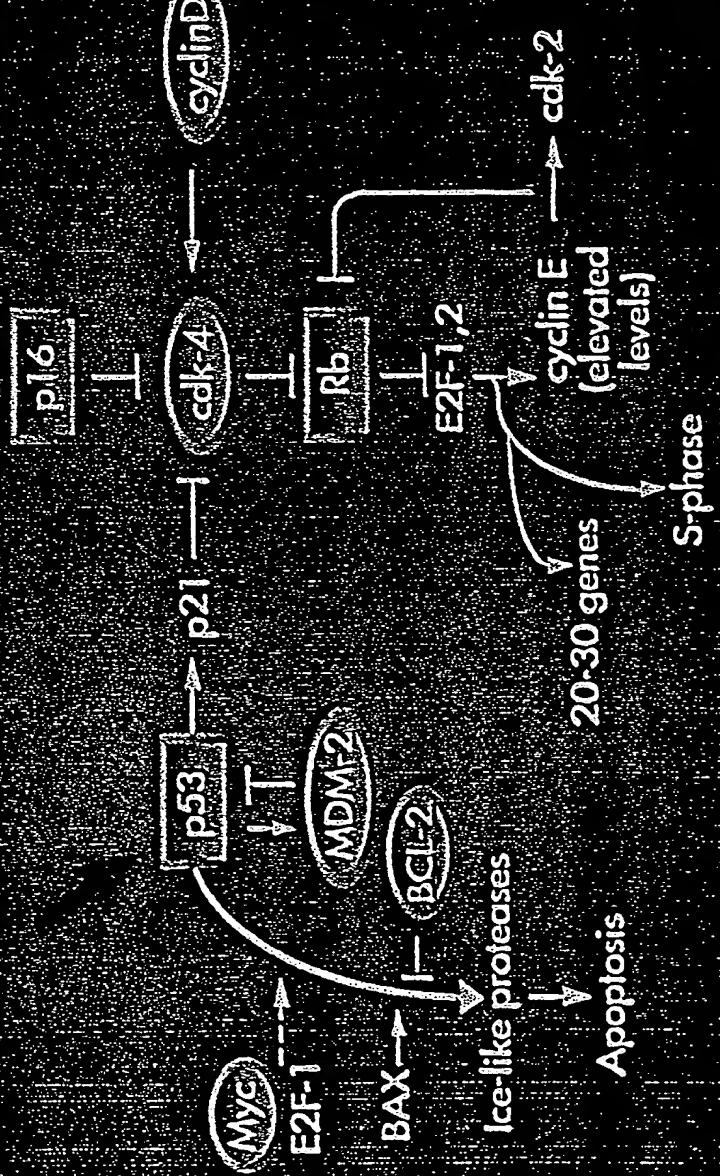


FIGURE 15

P53-Rb Pathway



00087234567890

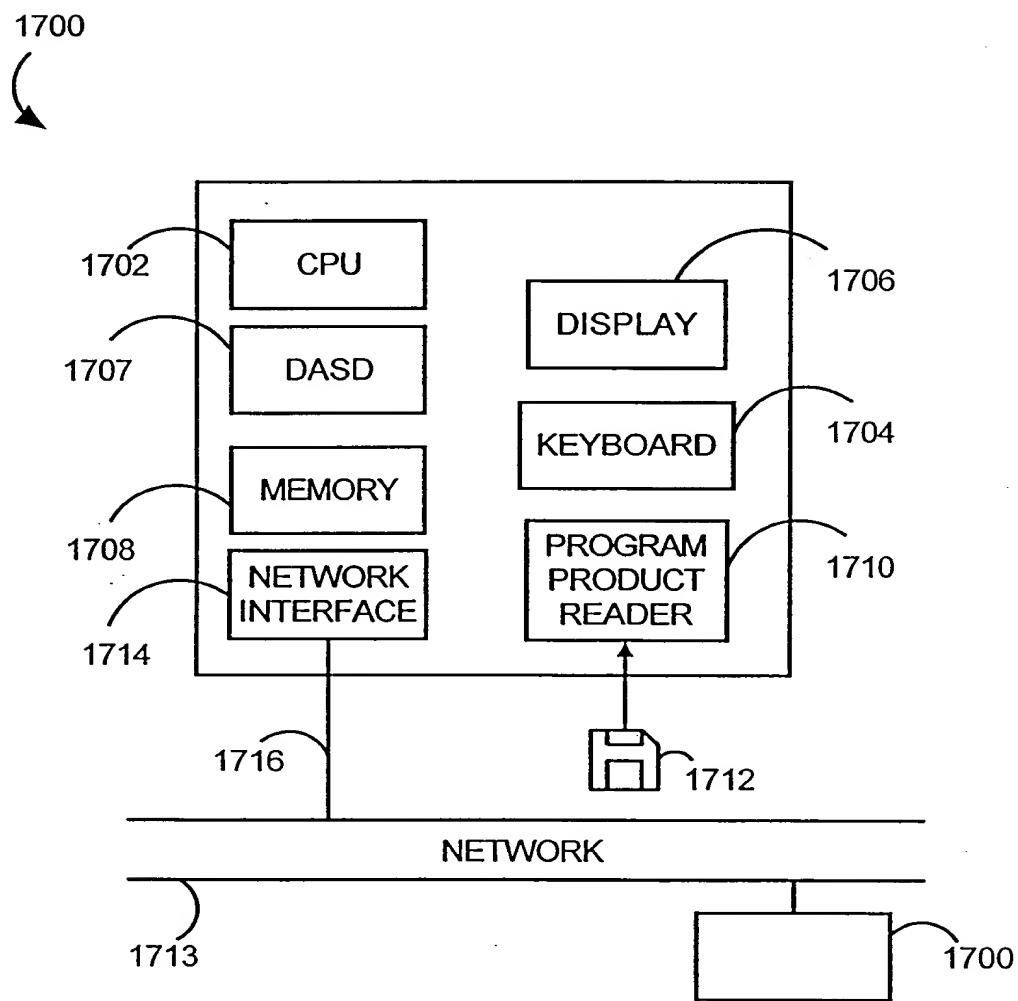


FIGURE 17

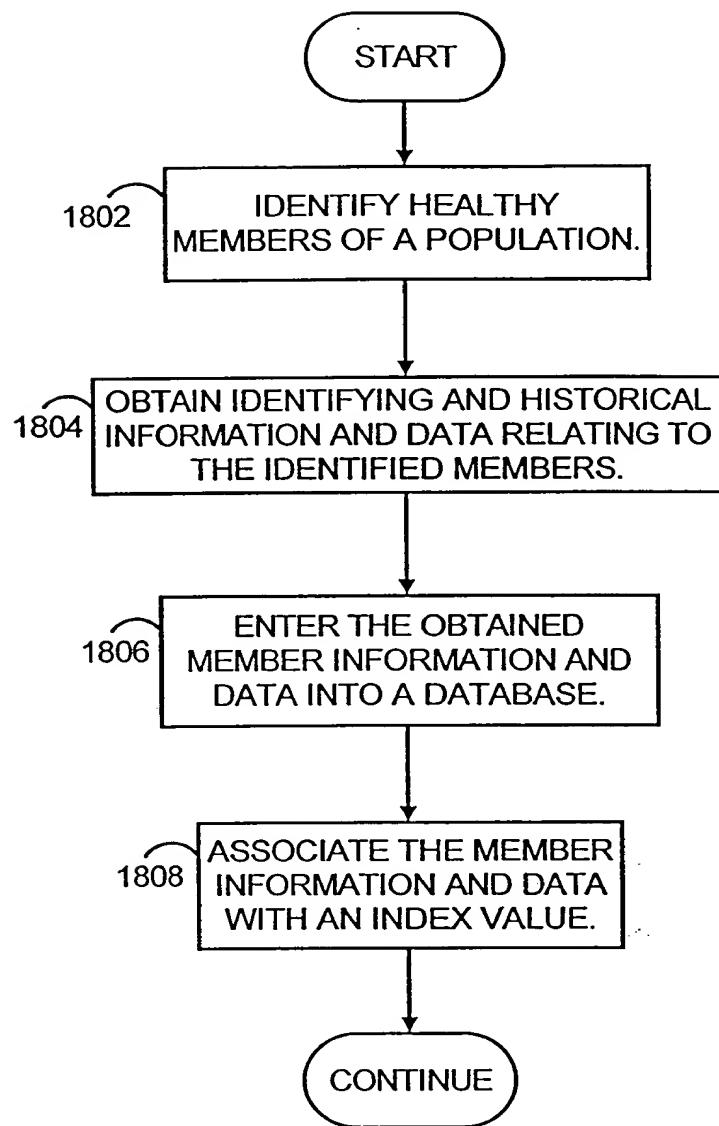


FIGURE 18

clone chromosome 17 (#48319)

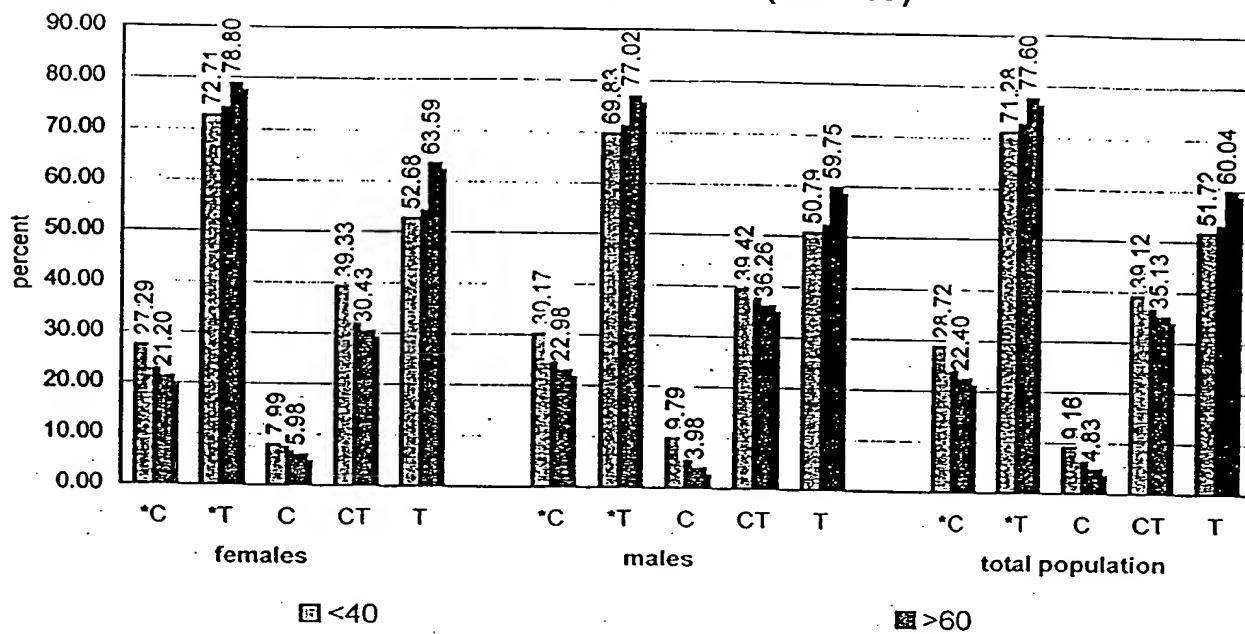


Figure 19

AKAP10 Ile646Val

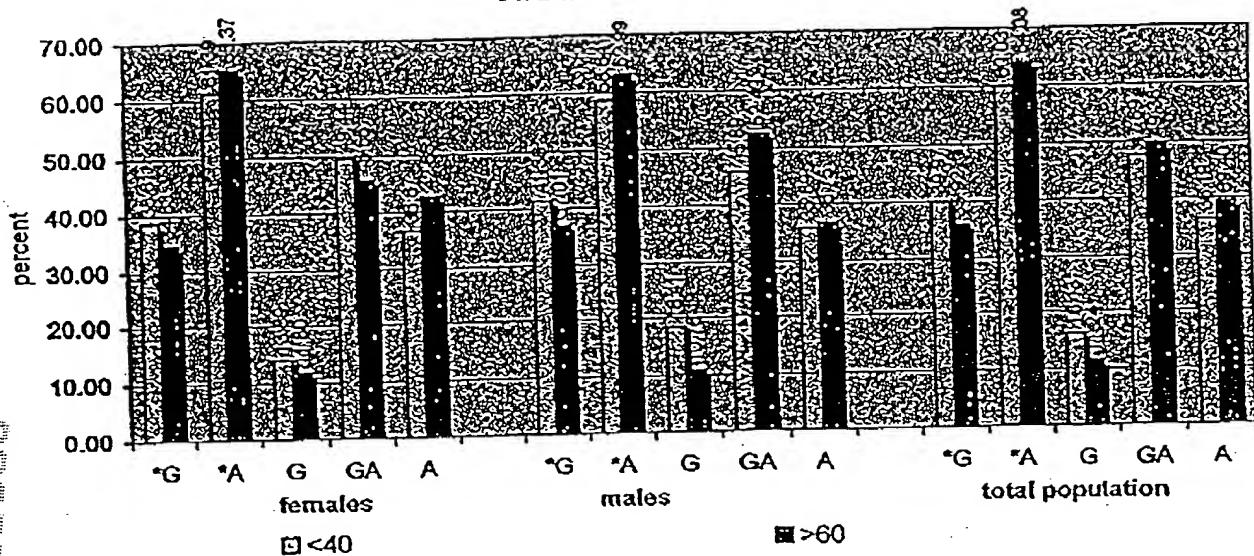


Figure 20

Figure 21

methionine sulfoxid reductase A (#63306)

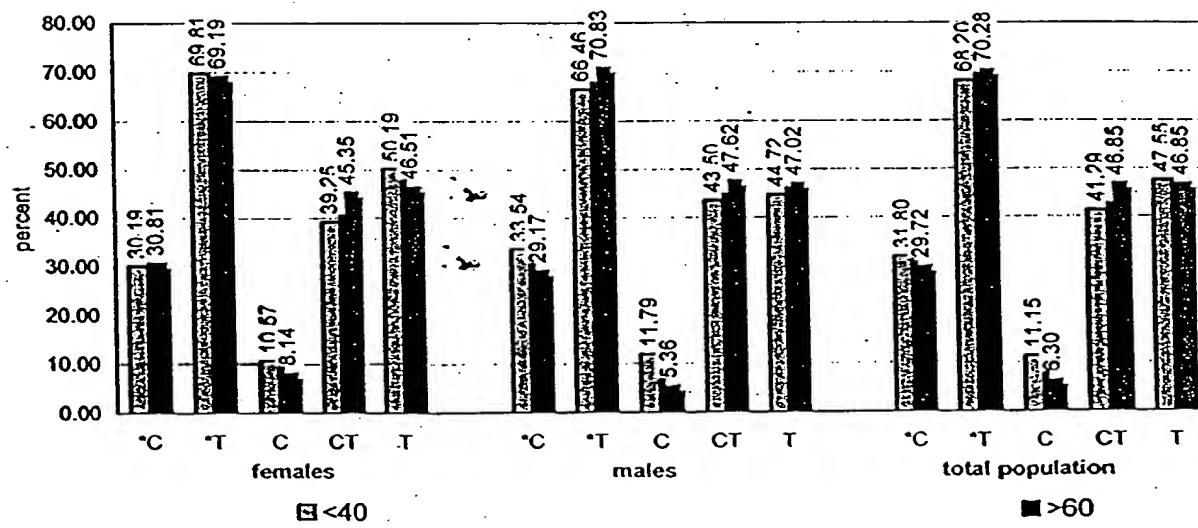
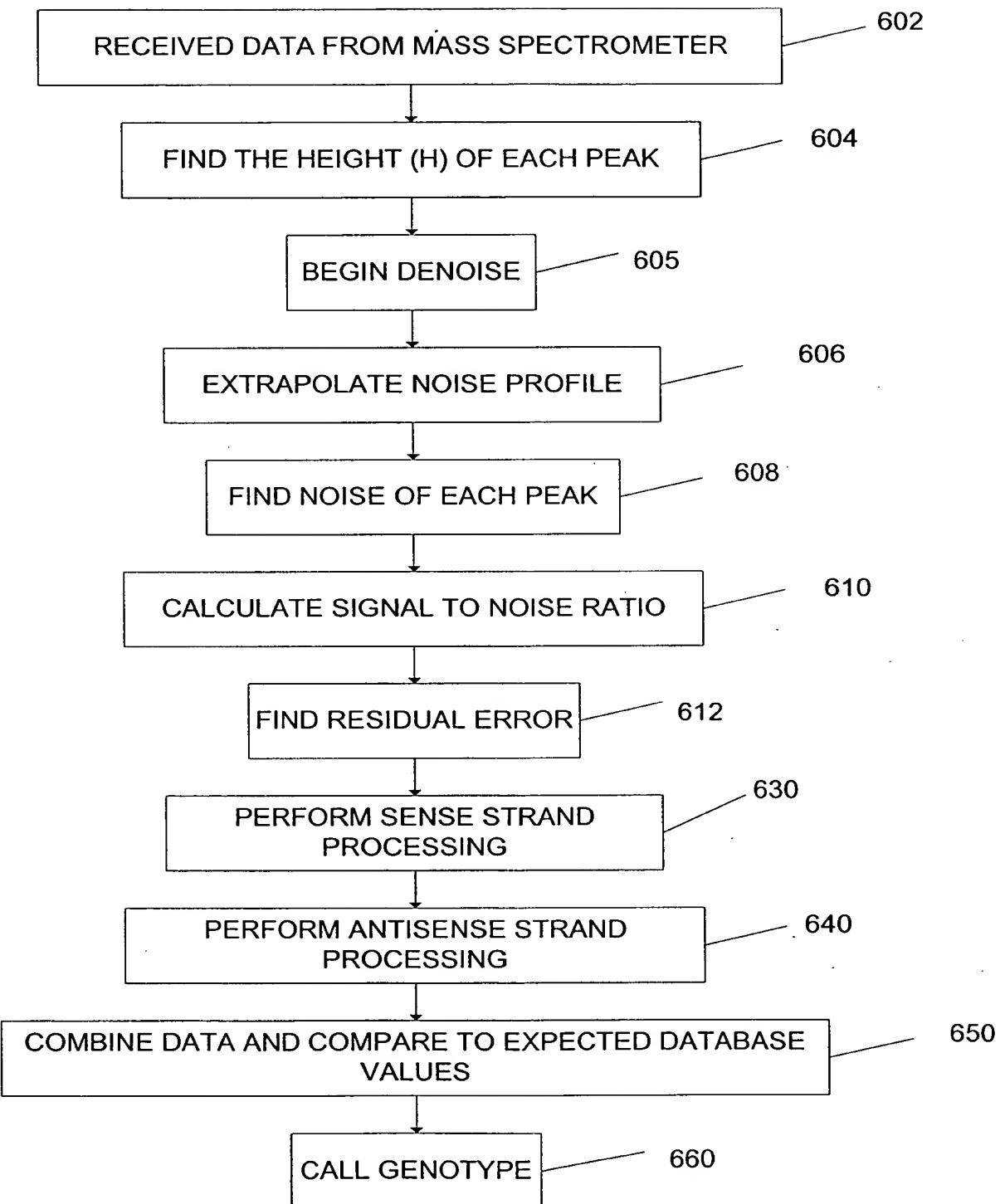


FIGURE 22A

**FIGURE 23**

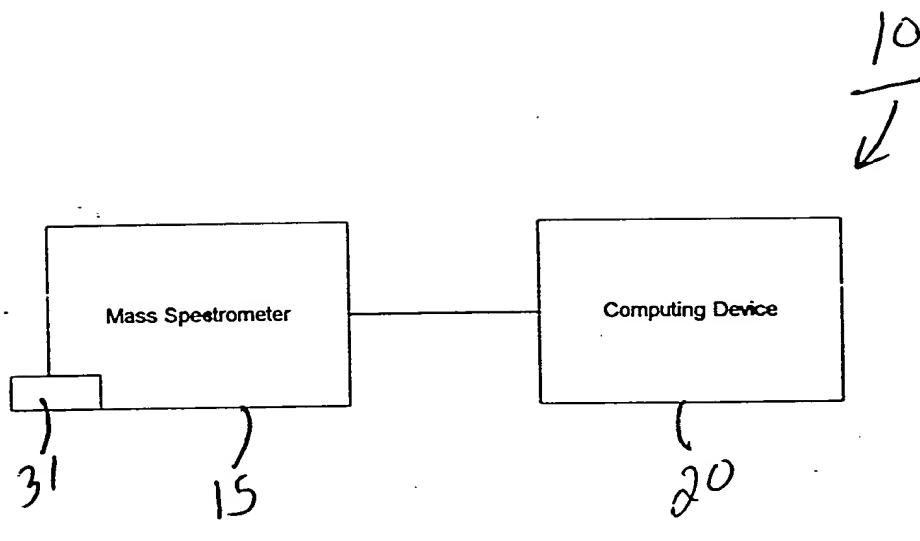
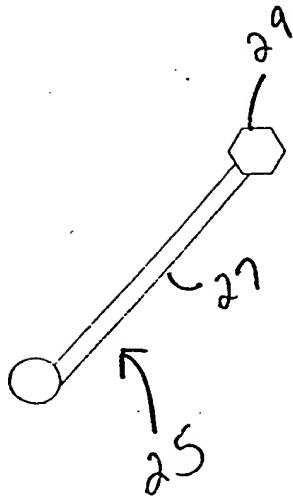


FIGURE 24

40

RECEIVE DATA

35

45

DENOISE

Wavelet Transformation

Noise Profile

Apply Noise Profile to each Stage

50

BASELINE
CORRECTION

Generate Sparse Data Set

Shift Signal

Generate Peak-Free Signal

Generate Baseline

Subtract Baseline From Signal

55

COMPRESSION

Mass Shift

Find width of Strongest Peak

Delete an Area Around Each Peak

Generate a Residual Baseline

Subtract Residual Baseline From Signal

Determine Height of Each Peak

Determine Peak Probabilities

Calling Genotypes

60

PEAK FITTING

65

GENOTYPE
CALLING

FIGURE 25

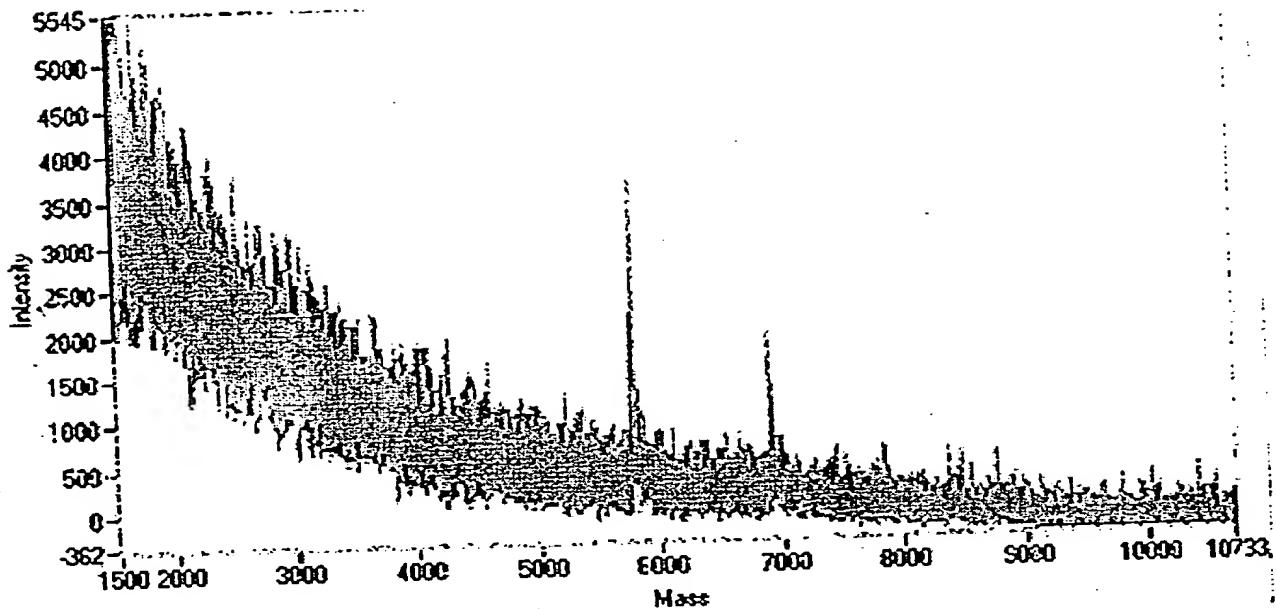


FIGURE 26

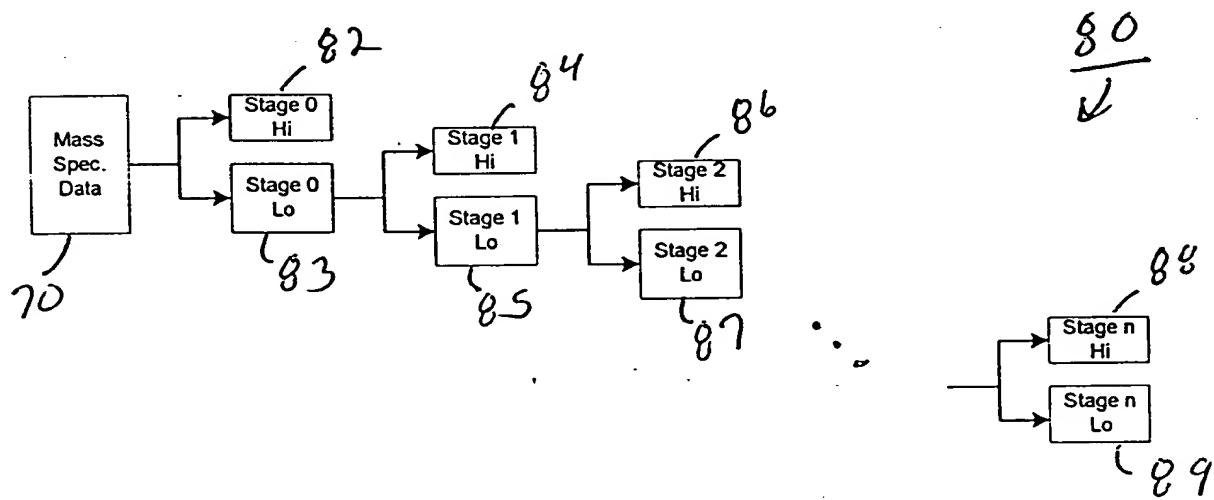


FIGURE 27

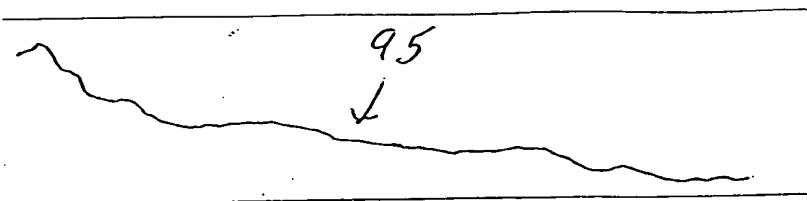
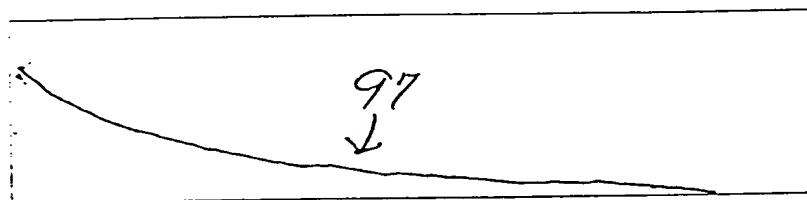


FIGURE 28



Exp fitting

FIGURE 29

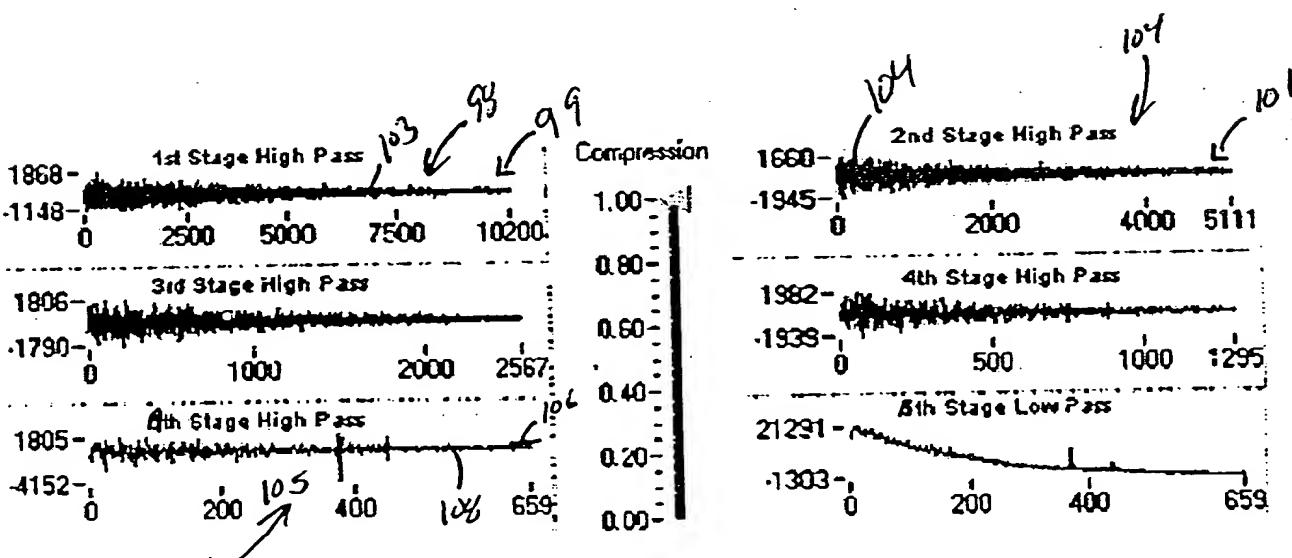


FIGURE 30

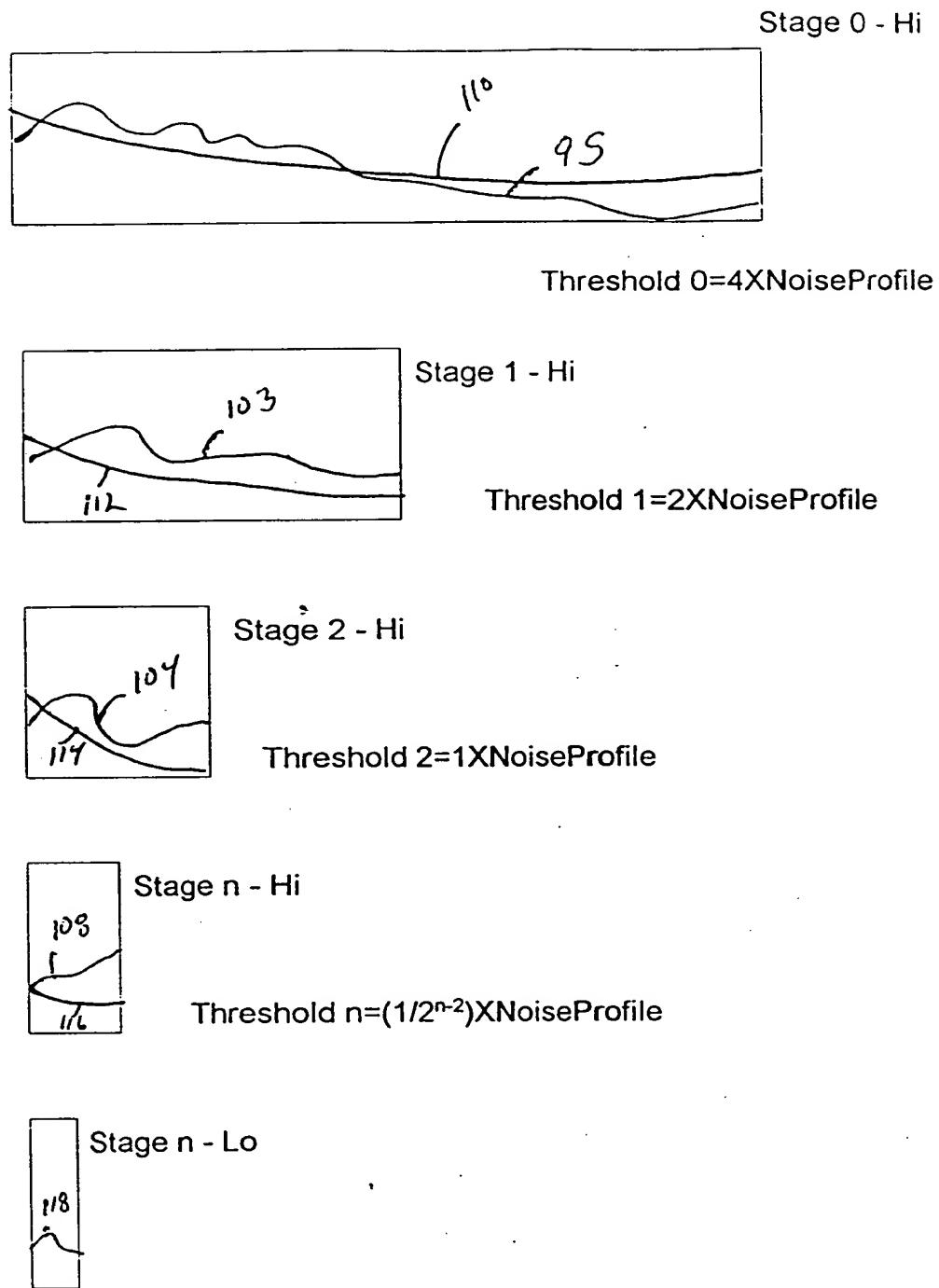


FIGURE 31

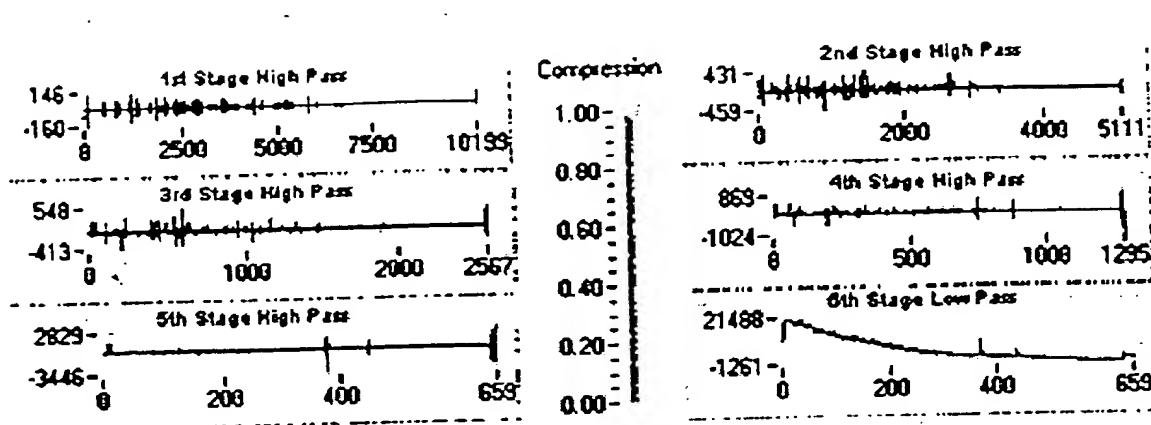


FIGURE 32

$$\text{Signal (t)} = \frac{(\text{Start } 0(t) + \text{Start } 1(t) + \text{Start } 2(t) \dots + \text{Start } 23(t))}{24}$$

FIGURE 33

SHIFT SIGNAL TO ACCOUNT FOR
VARIATIONS DUE TO STARTING POINT

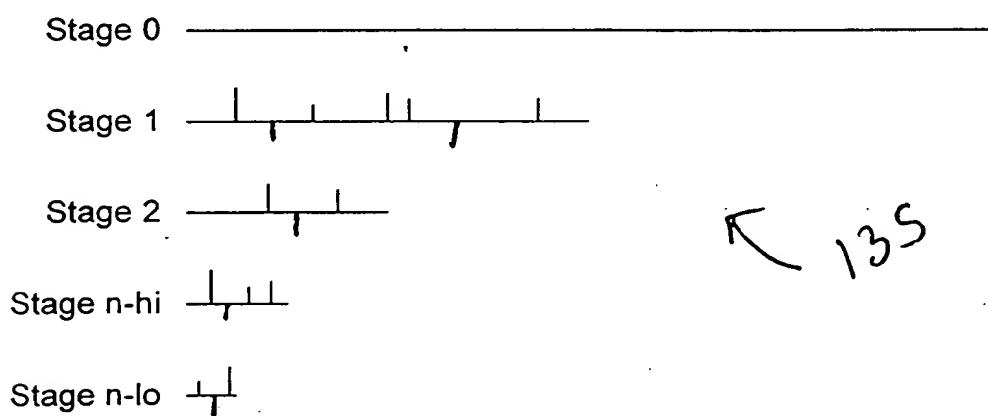


FIGURE 34

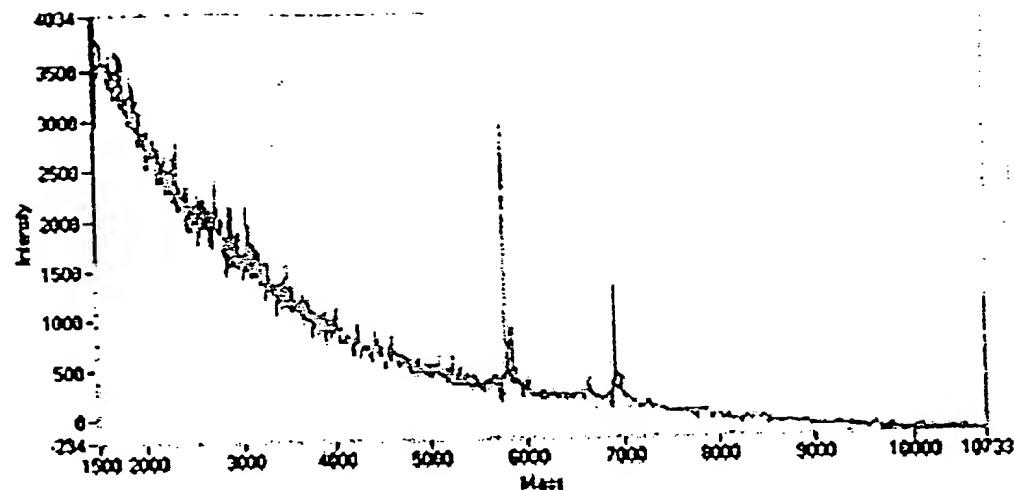


FIGURE 35

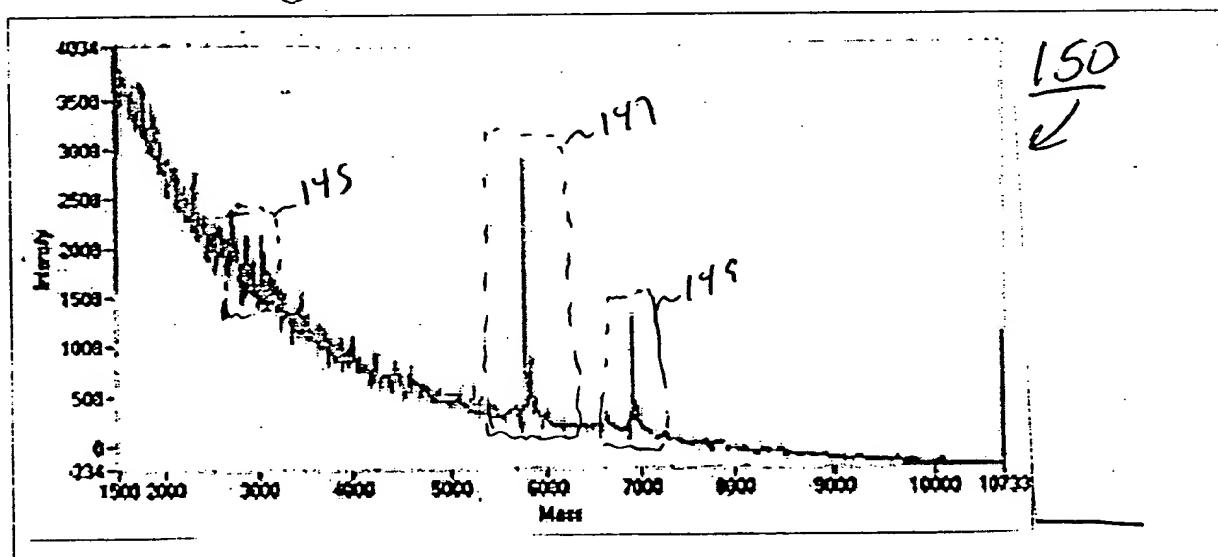


FIG. 13 - TAKE A MOVING AVERAGE, REMOVE SECTIONS EXCEDING A THRESHOLD

FIGURE 36

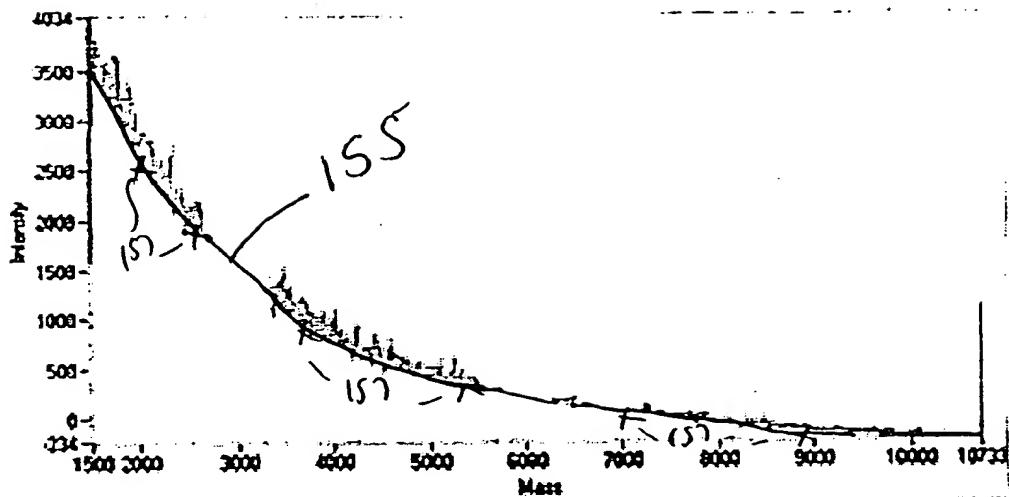


FIGURE 37

FIND MINIMA IN REMAINING SIGNALS AND CONNECT TO FORM A PEAK FREE SIGNAL

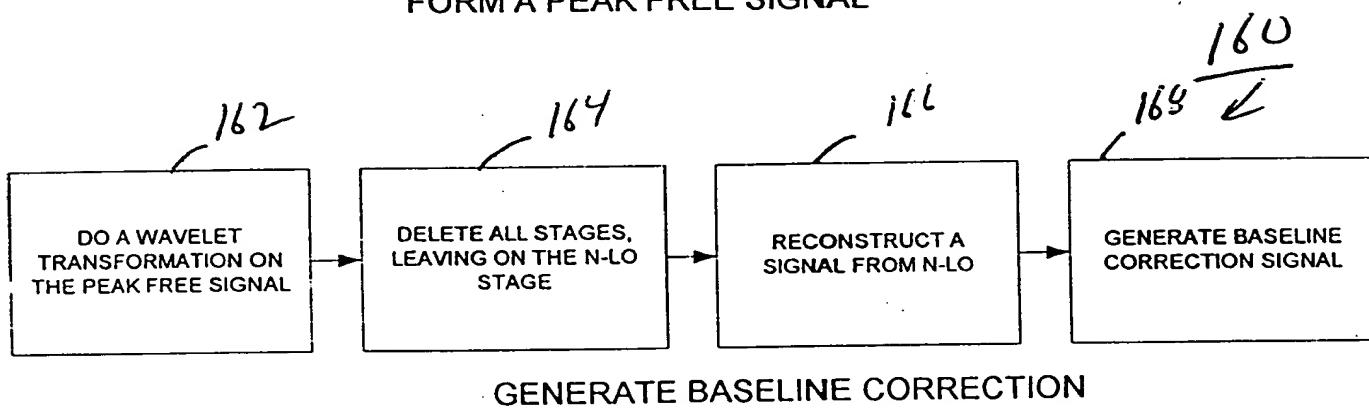


FIGURE 38

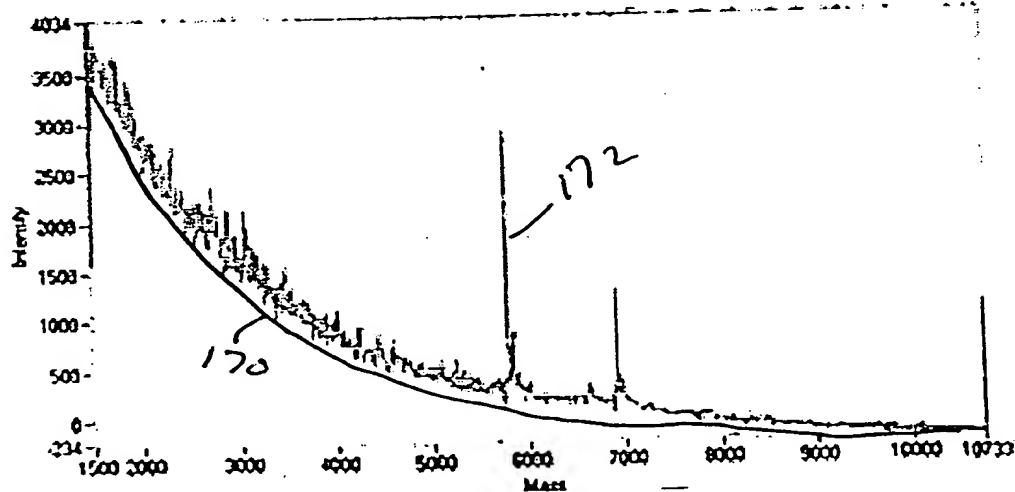


FIGURE 39

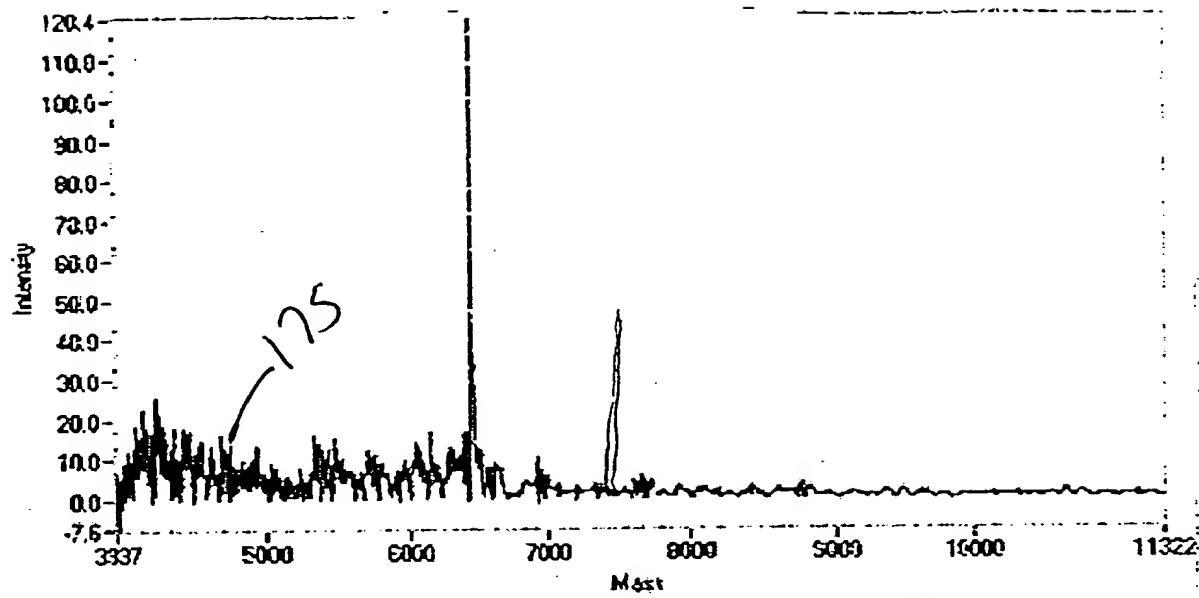


FIGURE 40

NON-0 COEFFICIENTS

NON-0 COEFFICIENTS	VALUE	194	195	196	198	199	100	RELATIVE
100	25							100.025
150	220							50.220
500	.1							350.0001
10,050	800							9550.8
10,075	890							25.89
11,125	910							150.91
12,100	1000 (MAX)							975.99999
13,250	940							1150.94

FIGURE 41

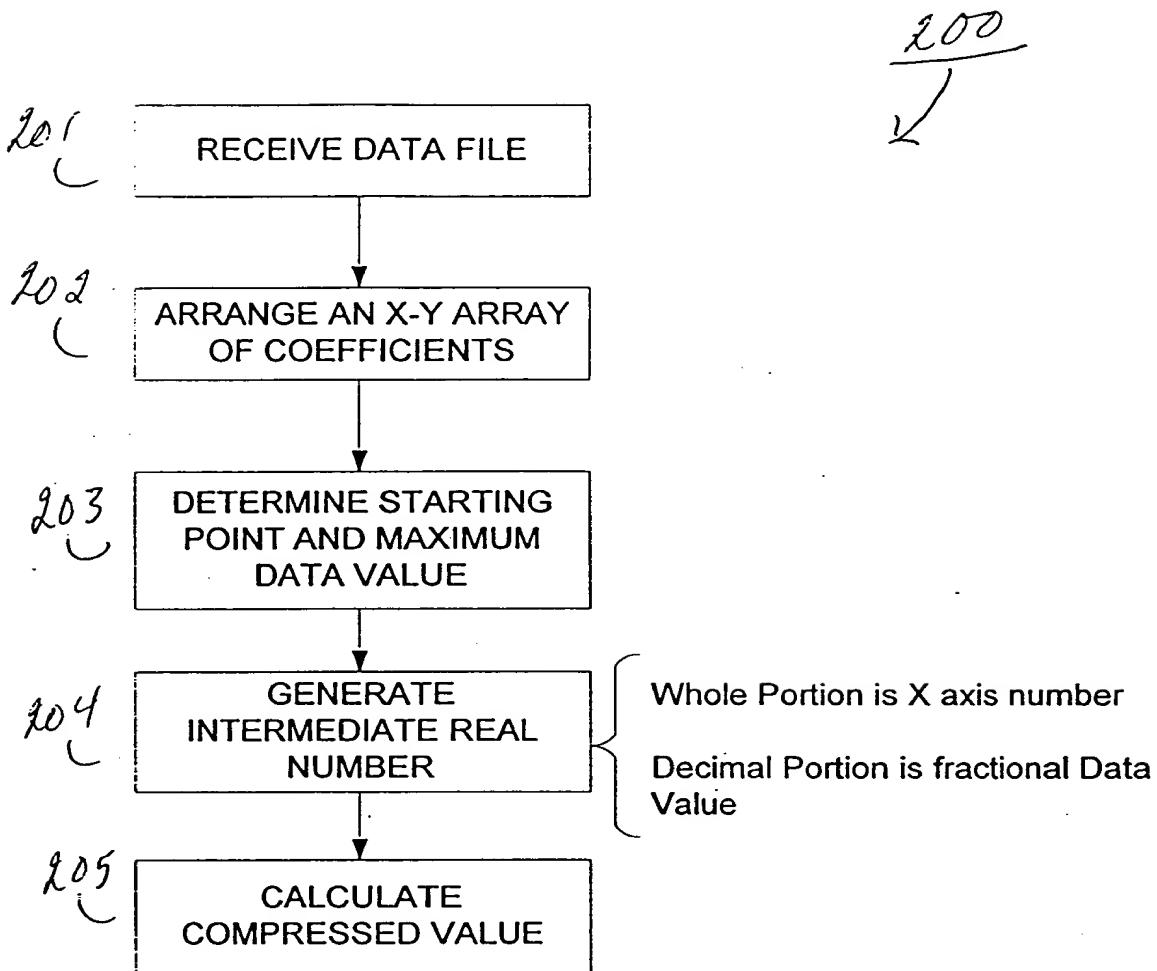


FIGURE 42

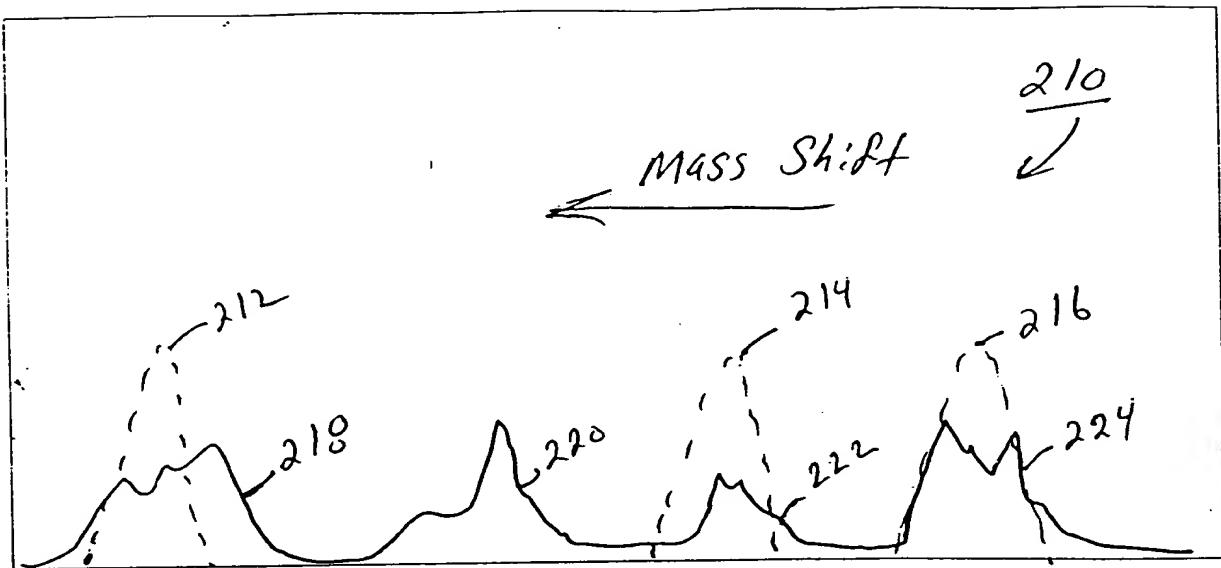


FIGURE 43

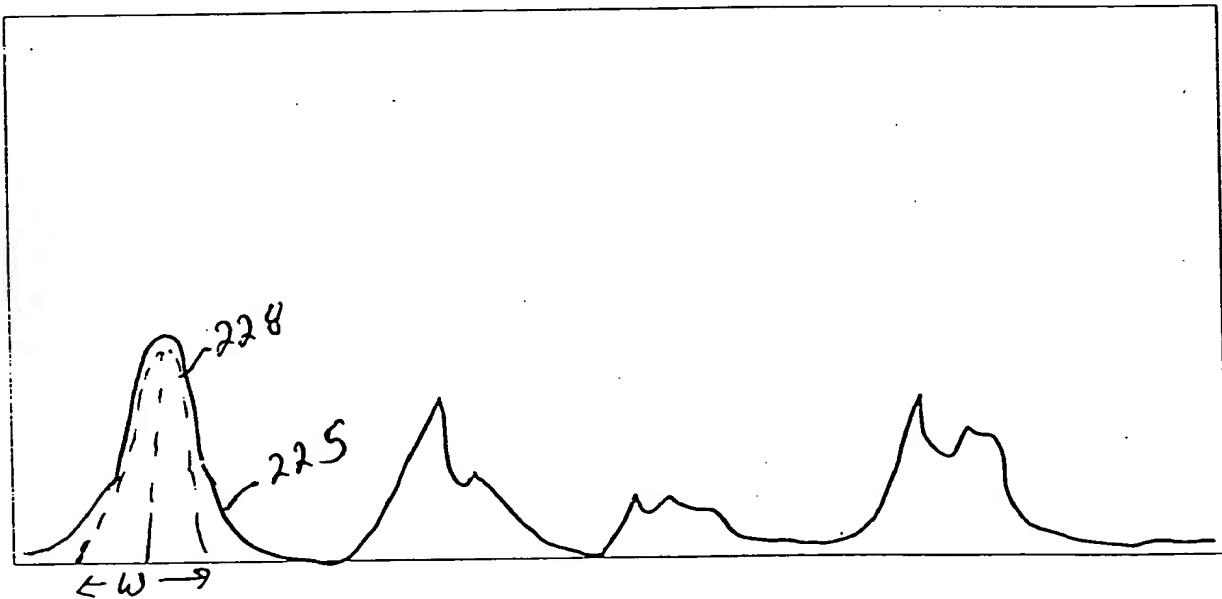


FIGURE 44

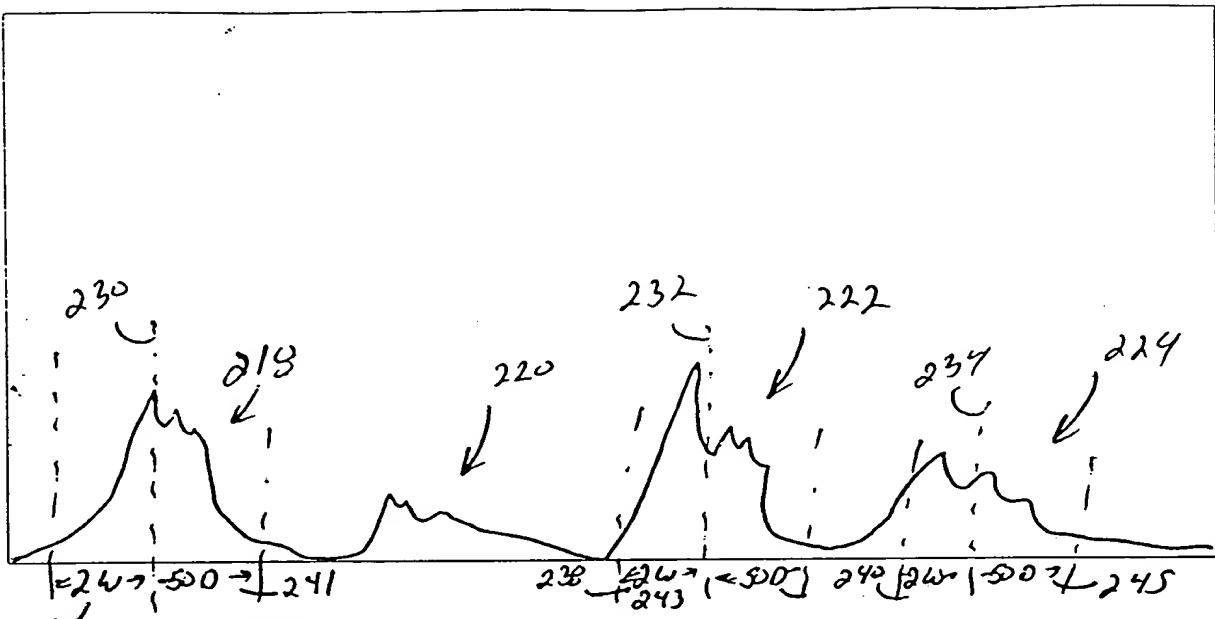


FIGURE 45

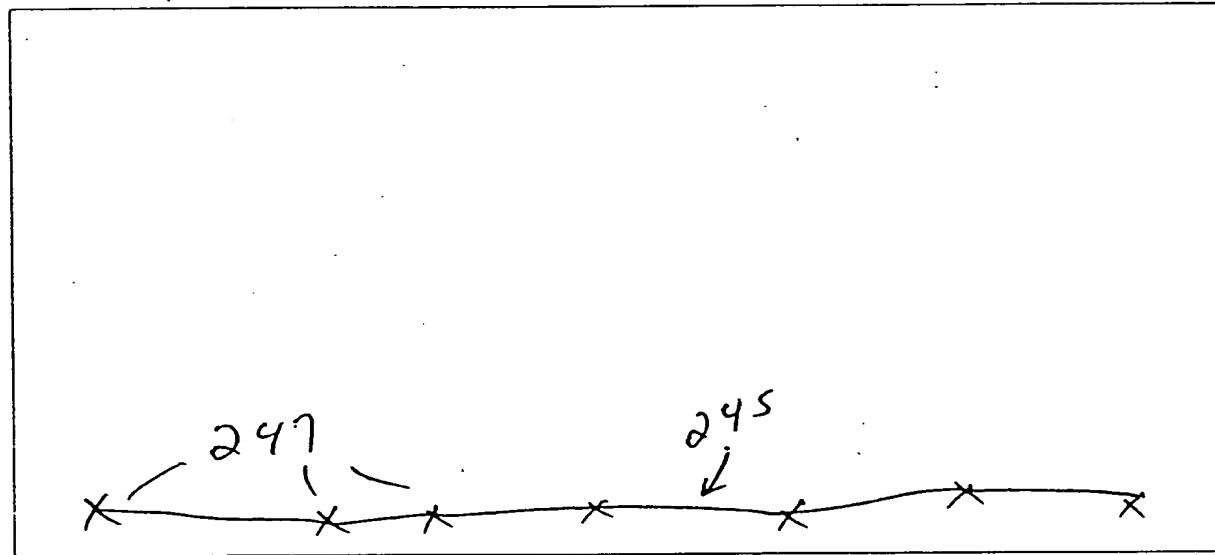


FIGURE 46

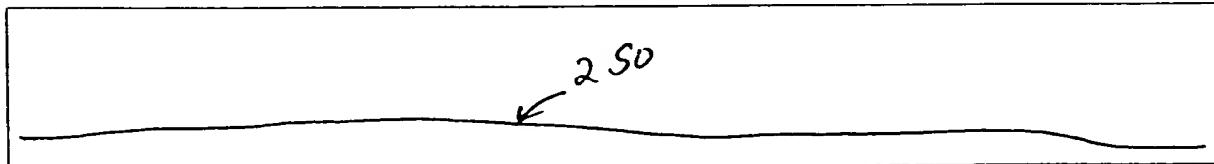


FIGURE 47

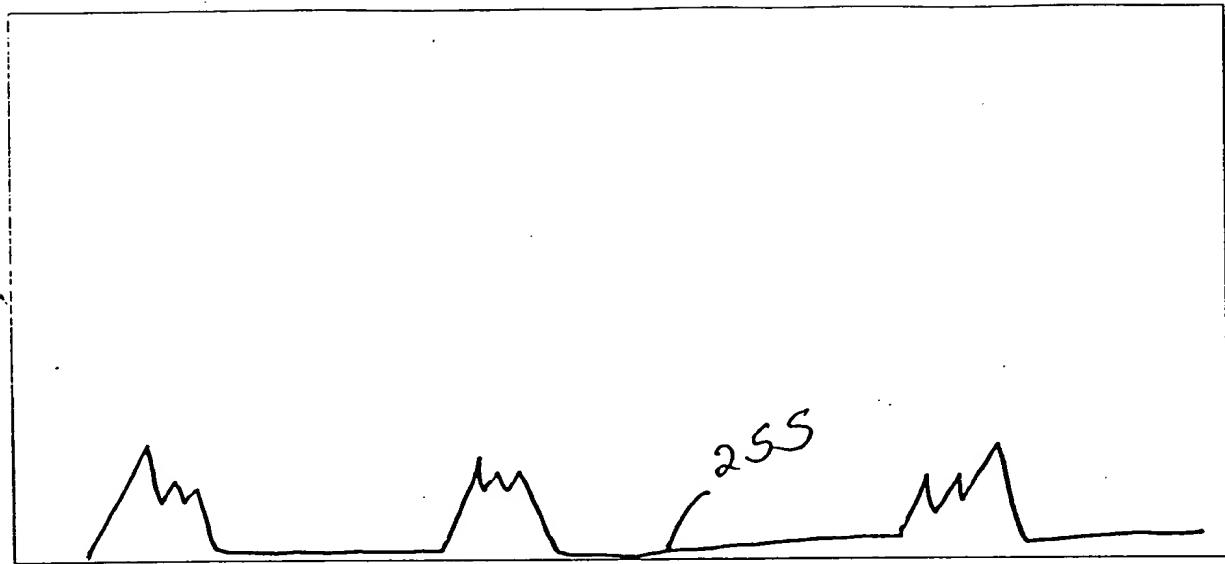


FIGURE 48

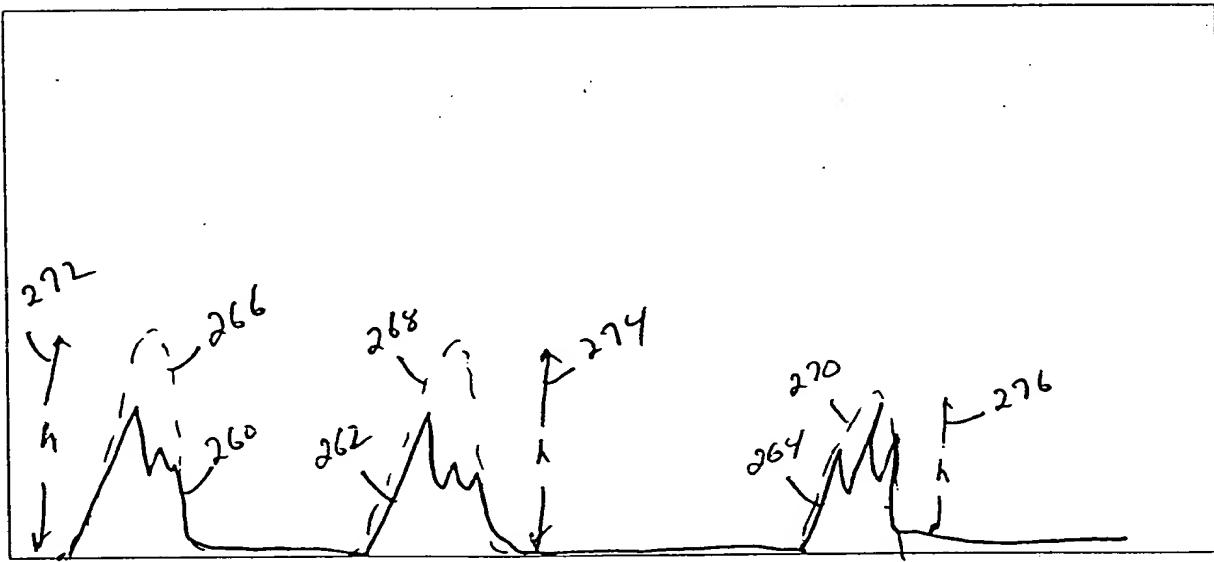


FIGURE 49

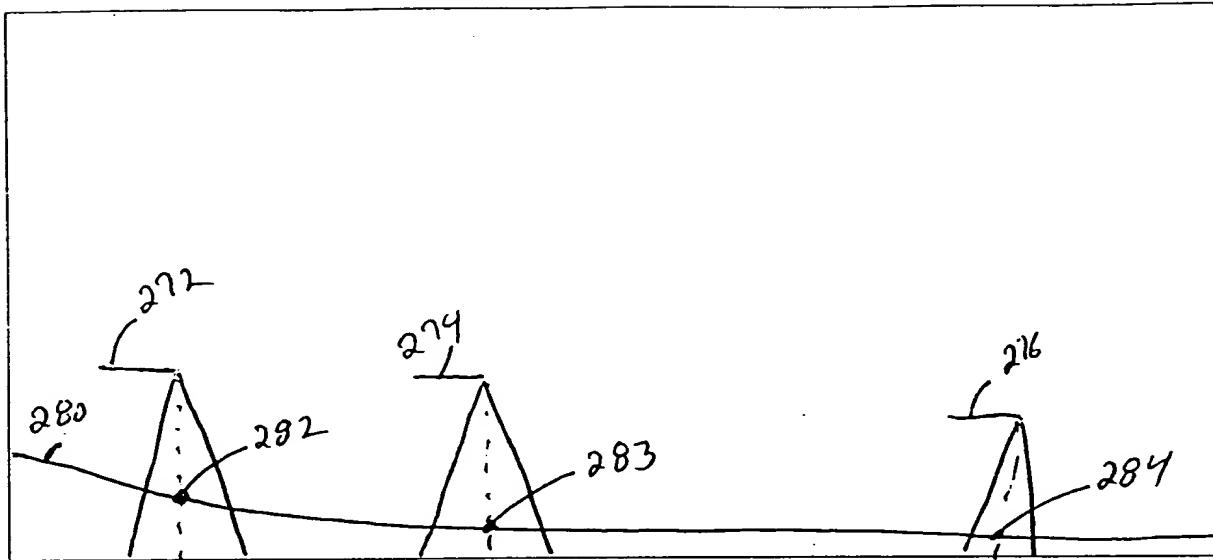


FIGURE 50

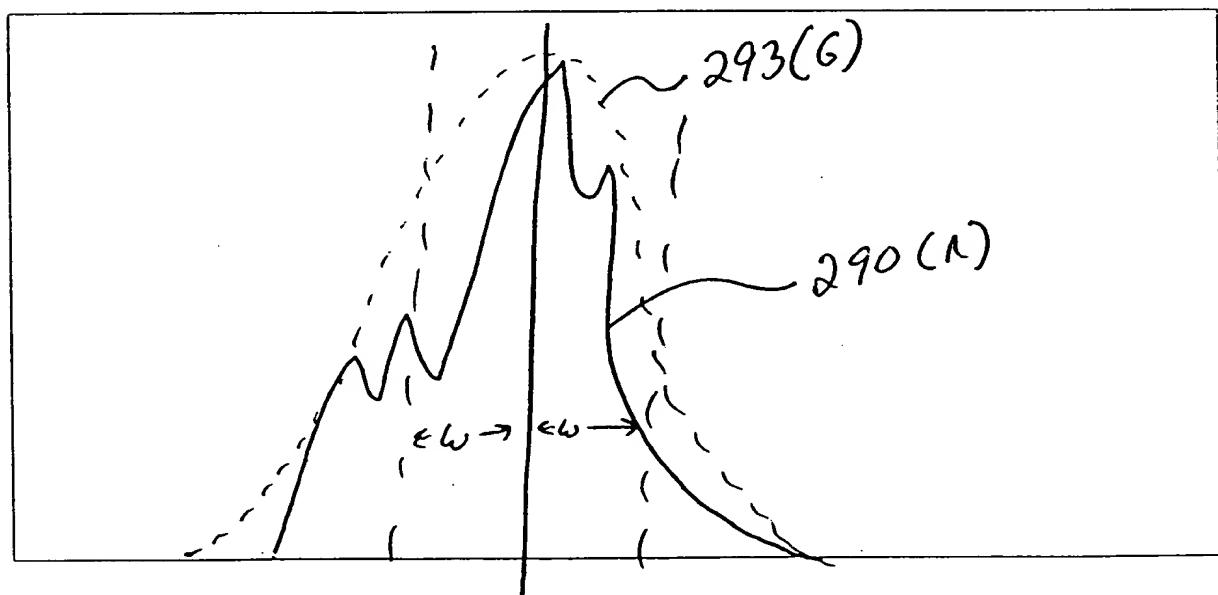


FIGURE 51

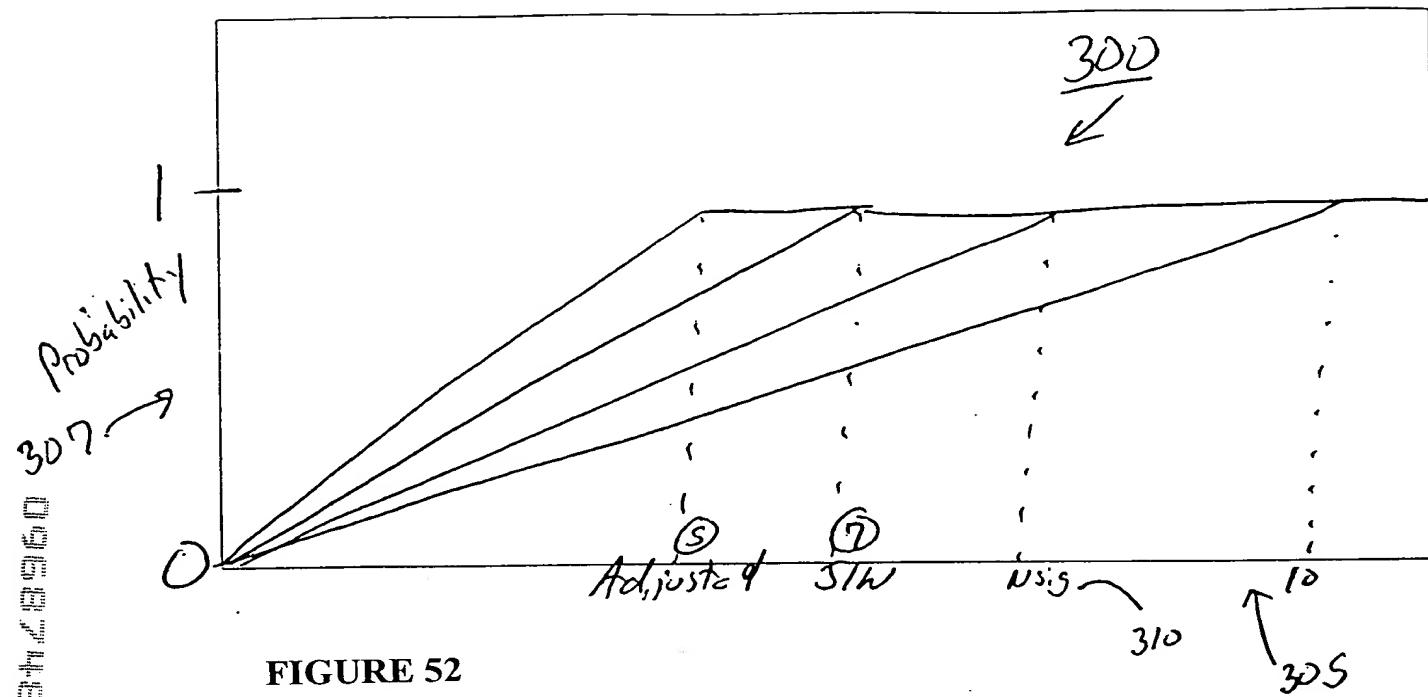


FIGURE 52

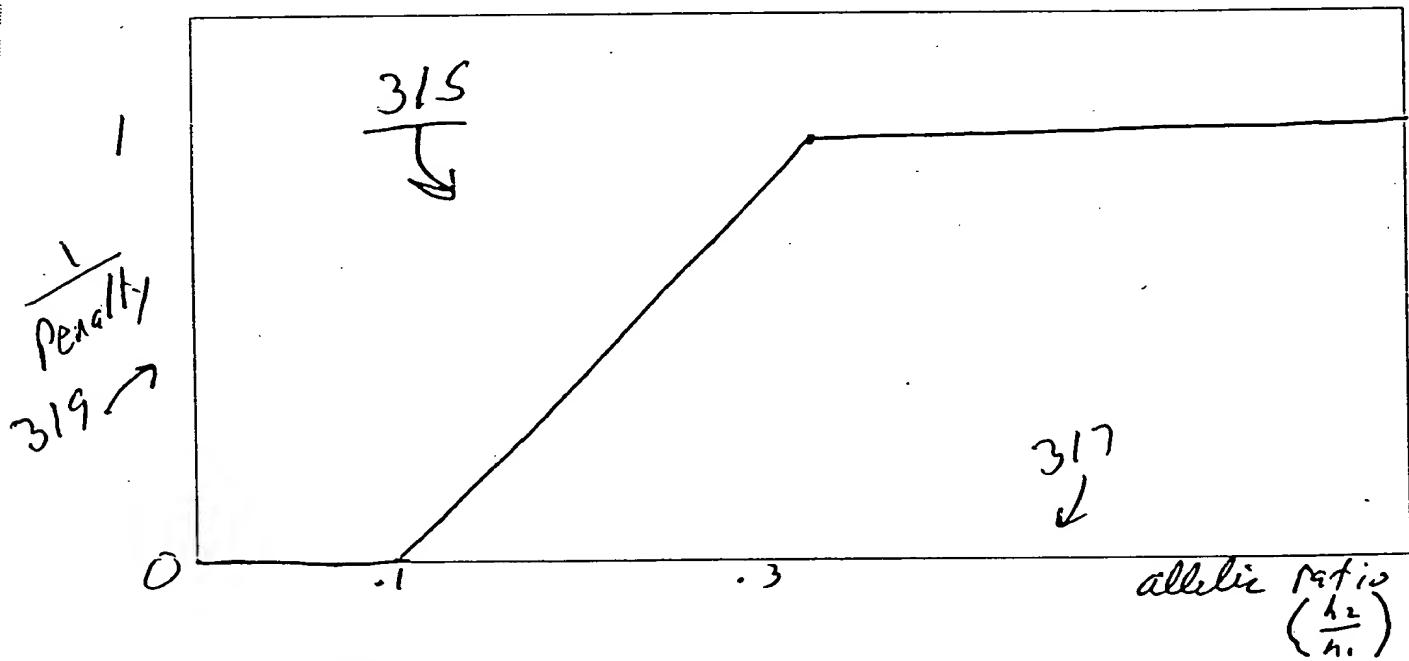


FIGURE 53

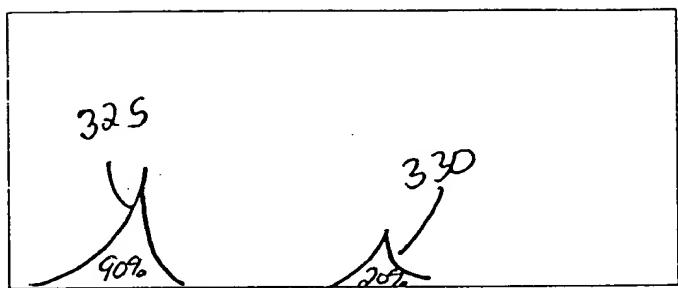


FIGURE 54

329

PROBABILITY OF GG EXISTING:
 $P(GG) = P(G) * P(1-C)$
 $= 90\% * (100\% - 20\%)$
 $= 90\% * 80\%$
 $= 72\%$

331

PROBABILITY OF CC EXISTING:
 $P(CC) = P(C) * P(1-G)$
 $= 20\% * (100\% - 90\%)$
 $= 20\% * 10\%$
 $= 2\%$

333

PROBABILITY OF GC EXISTING:
 $P(GC) = P(G) * P(C)$
 $= 90\% * 20\%$
 $= 18\%$

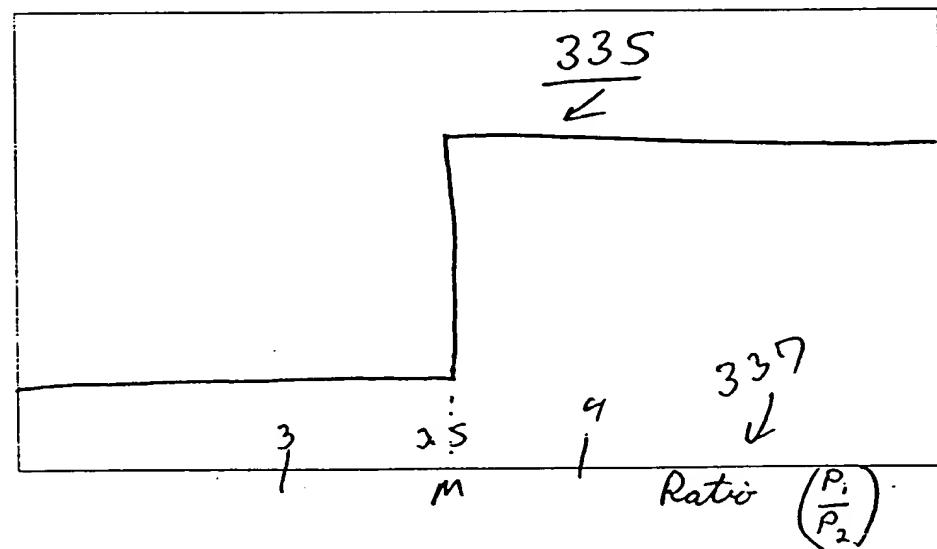


FIGURE 55

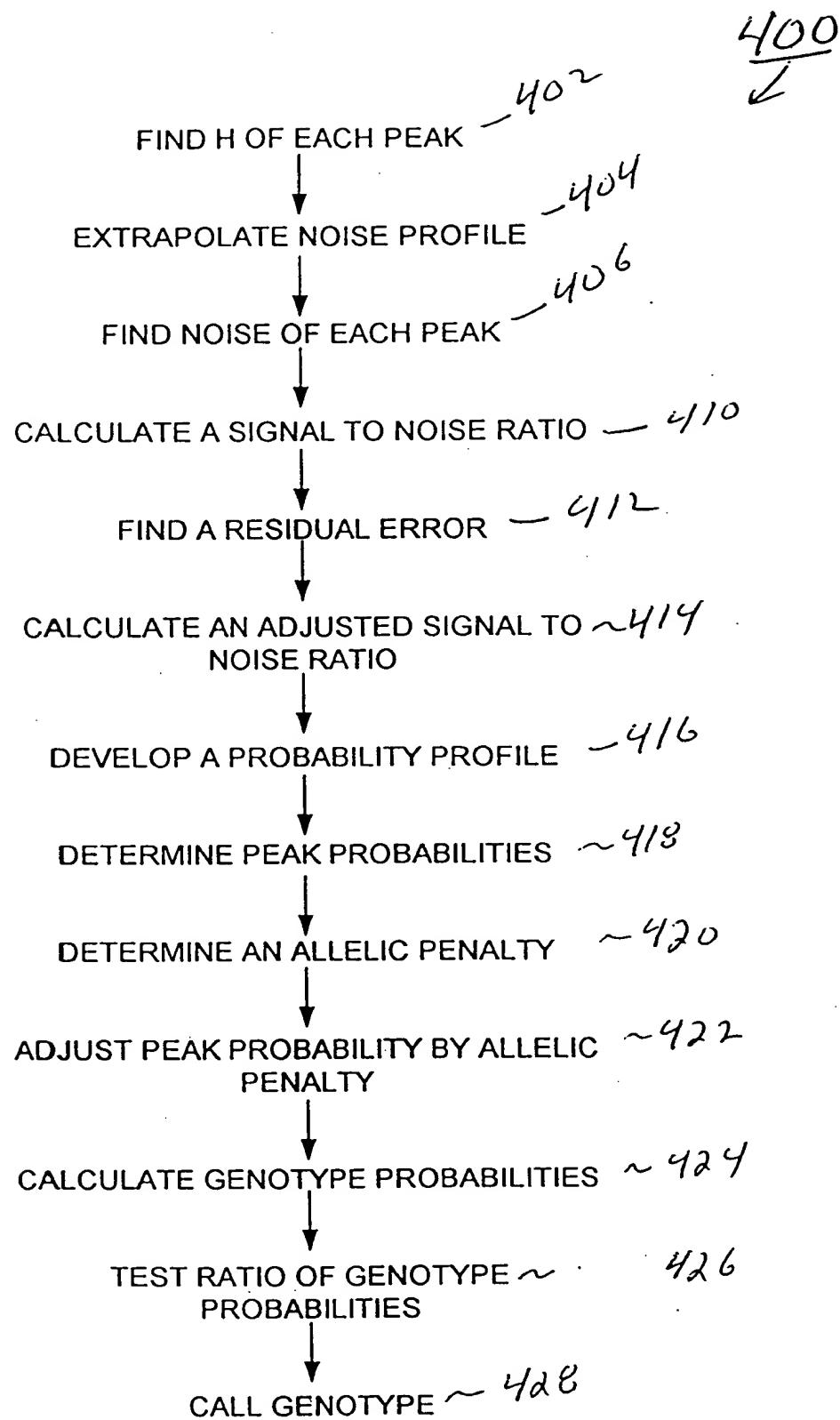


FIGURE 56

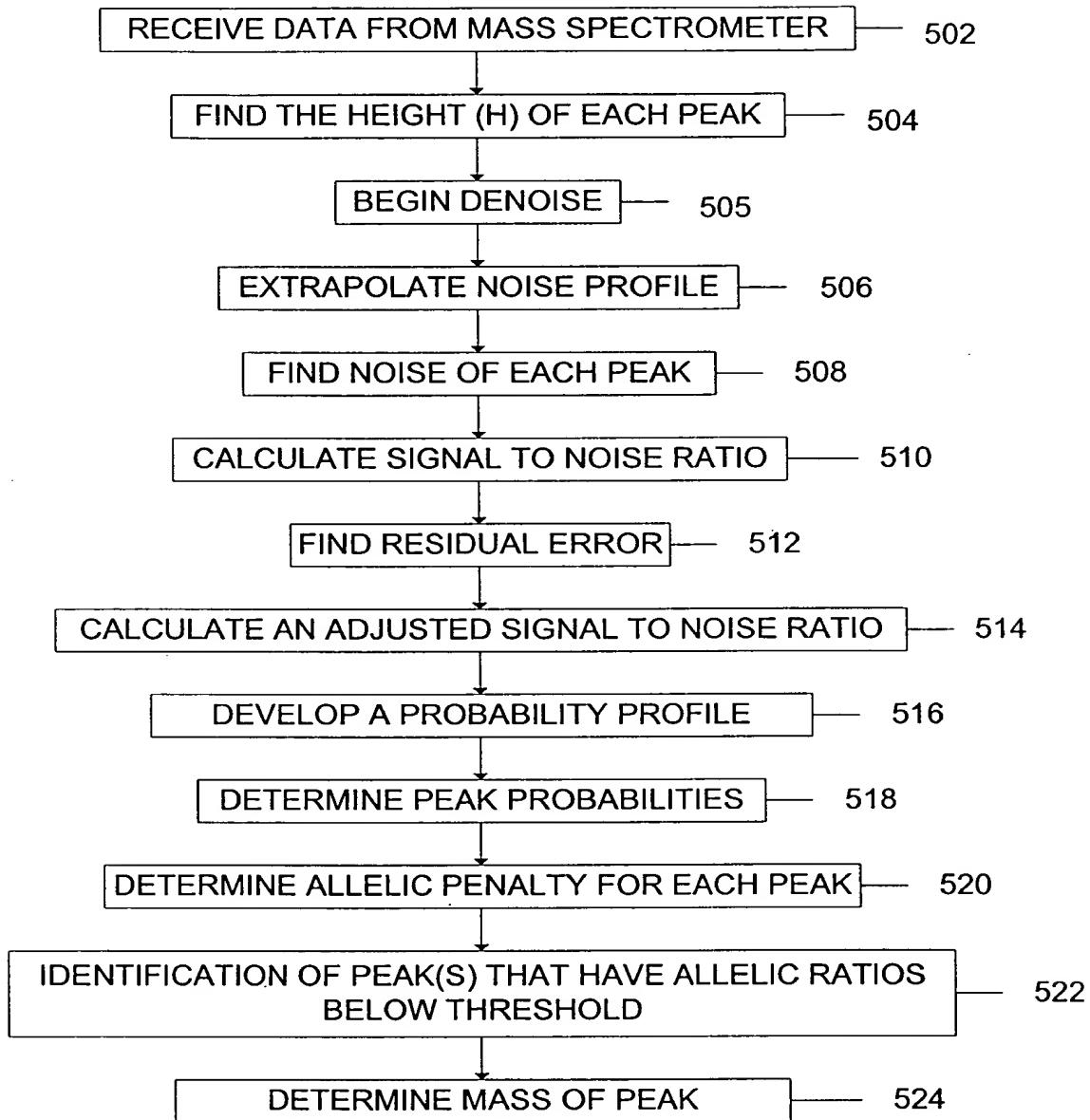


FIGURE 57

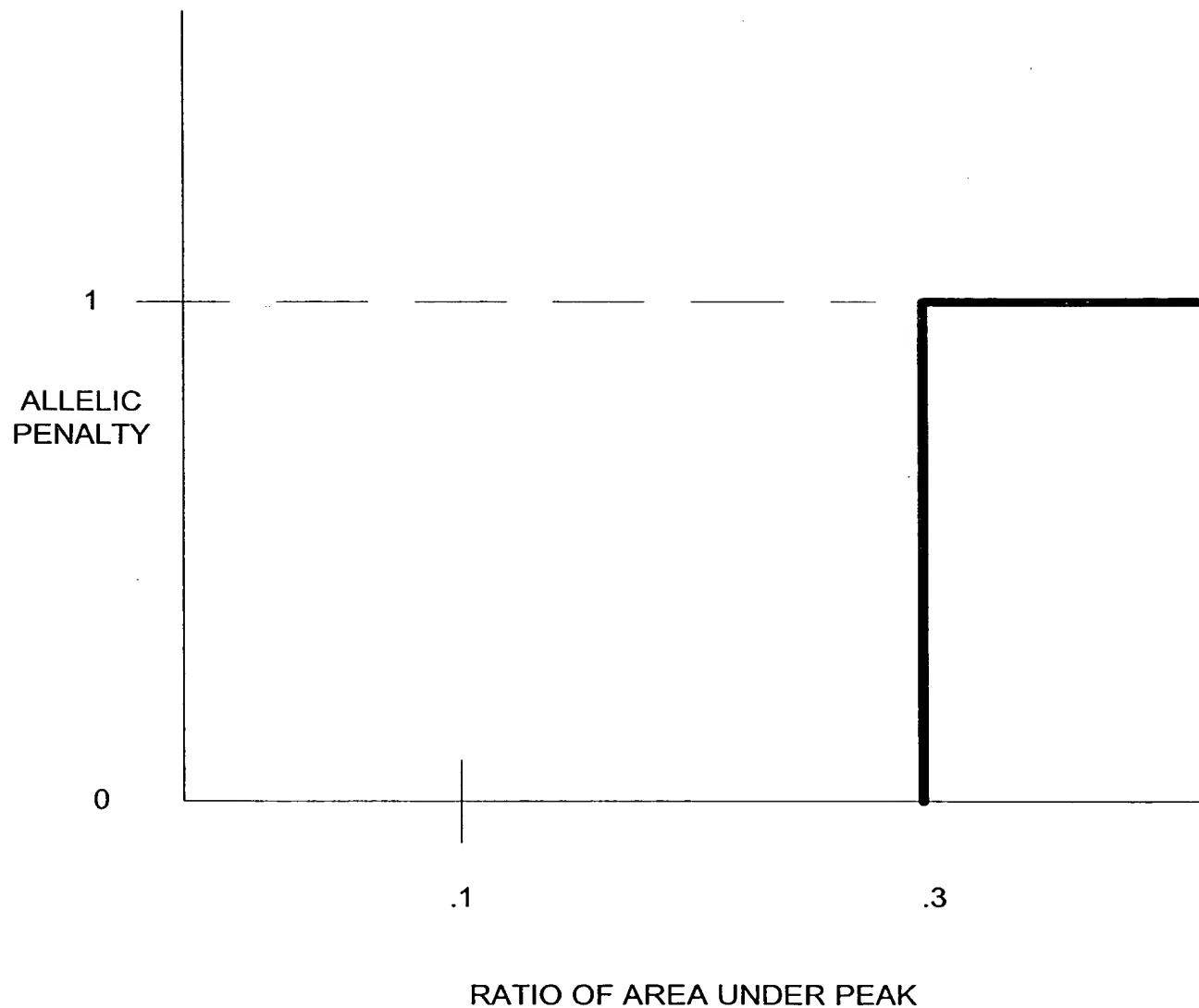


FIGURE 58